GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:10:27 ; Search time 15 Seconds
(without alignments)
32.045 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	9	2	A24244	adipokinetic hormo
2	17	85.0	53	2	T00172	hypothetical prote
3	17	85.0	53	2	D89989	hypothetical prote
4	17	85.0	63	2	T29202	hypothetical prote
5	17	85.0	65	1	A32613	adipokinetic hormo
6	17	85.0	67	2	T12860	hypothetical prote
7	17	85.0	70	2	A86942	hypothetical prote
8	17	85.0	72	2	S15137	thioredoxin h2 - s
9	17	85.0	77	2	S18581	pufQ protein - Rho
10	17	85.0	77	2	T50756	pufQ protein [impo
11	17	85.0	84	2	E69268	hypothetical prote
12	17	85.0	88	2	B46264	thioredoxin 2 - sl
13	17	85.0	98	2	F47624	Ig heavy chain V-I
14	17	85.0	99	2	S37447	gene E2 protein -
15	17	85.0	99	2	S37448	gene E2 protein -
16	17	85.0	99	2	S37441	gene E2 protein -
17	17	85.0	99	2	S37442	gene E2 protein -
18	17	85.0	99	2	S37444	gene E2 protein -
19	17	85.0	102	2	G71043	hypothetical prote
20	17	85.0	102	2	B56956	GTP-binding protei
21	17	85.0	104	1	A28086	thioredoxin - rabb
22	17	85.0	105	1	JH0568	thioredoxin [valid
23	17	85.0	105	1	JS0667	thioredoxin - rhes
24	17	85.0	105	1	S04352	thioredoxin - rat
25	17	85.0	105	1	S04107	thioredoxin - mous
26	17	85.0	105	1	A30006	thioredoxin - chic
27	17	85.0	107	2	T33843	hypothetical prote
28	17	85.0	108	2	AH2101	thioredoxin [impor
29	17	85.0	112	2	PH0980	Ig heavy chain V r
30	17	85.0	112	2	AF2549	hypothetical prote
31	17	85.0	113	1	S57775	thioredoxin h, cyt
32	17	85.0	114	1	JQ2242	thioredoxin h - Ar
33	17	85.0	115	1	G3HUJN	Ig heavy chain V-I
34	17	85.0	115	2	PL0238	Ig heavy chain V r
35	17	85.0	115	2	G72642	probable surface p
36	17	85.0	116	2	T10739	thioredoxin - comm
37	17	85.0	117	2	PL0237	Ig heavy chain V r
38	17	85.0	117	2	PL0235	Ig heavy chain V r
39	17	85.0	117	2	PL0234	Ig heavy chain V r
40	17	85.0	118	1	S34812	thioredoxin h2 - c
41	17	85.0	118	2	T10170	thioredoxin - cast
42	17	85.0	118	2	S58118	thioredoxin (clone
43	17	85.0	118	2	S58120	thioredoxin (clone
44	17	85.0	118	2	PL0231	Ig heavy chain V r
45	17	85.0	118	2	F82424	diacylglycerol kin

ALIGNMENTS

RESULT 1
A24244
adipokinetic hormone - bollworm
N;Alternate names: Hez-AKH
C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C;Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C;Accession: A24244
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridg
Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of He
A;Reference number: A24244; MUID:86186794; PMID:3964263
A;Accession: A24244
A;Molecule type: protein
A;Residues: 1-9 <JAF>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 85.0%; Score 17; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 FXXXW 5
           |   |
Db       4 FTSSW 8
```

RESULT 2
T00172
hypothetical protein 38 - Staphylococcus aureus phage phi PVL
C;Species: Staphylococcus aureus phage phi PVL
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: T00172
R;Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.
Biosci. Biotechnol. Biochem. 61, 1960-1962, 1997
A;Title: Panton-Valentine leukocidin genes in a phage-like particle isolated from mit
A;Reference number: Z14119; MUID:98067870; PMID:9404084
A;Accession: T00172
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-53 <KAN>
A;Cross-references: EMBL:AB009866; NID:d1204727; PIDN:BAA31912.1; PID:d1032873

Query Match 85.0%; Score 17; DB 2; Length 53;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 FXXXW 5
           |   |
Db      28 FTTAW 32
```

RESULT 3
D89989
hypothetical protein SAS063 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: D89989
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89989
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-53 <KUR>
A;Cross-references: GB:BA000018; PID:g13701784; PIDN:BAB43077.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SAS063

Query Match 85.0%; Score 17; DB 2; Length 53;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 28 FTTAW 32

RESULT 4
T29202
hypothetical protein F28F9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29202
R;Nelson, J.; Wohldmann, P.
submitted to the EMBL Data Library, September 1996
A;Description: The sequence of C. elegans cosmid F28F9.
A;Reference number: Z20587
A;Accession: T29202
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-63 <NEL>
A;Cross-references: EMBL:U70850; PIDN:AAB09124.1; GSPDB:GN00022; CESP:F28F9.3
A;Experimental source: strain Bristol N2; clone F28F9
C;Genetics:
A;Gene: CESP:F28F9.3
A;Map position: 4
A;Introns: 38/1

Query Match 85.0%; Score 17; DB 2; Length 63;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 30 FATAW 34

RESULT 5
A32613
adipokinetic hormone precursor - tobacco hornworm
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1999
C;Accession: A32613
R;Bradfield, J.Y.; Keeley, L.L.
J. Biol. Chem. 264, 12791-12793, 1989
A;Title: Adipokinetic hormone gene sequence from Manduca sexta.
A;Reference number: A32613; MUID:89327232; PMID:2753887
A;Accession: A32613
A;Molecule type: DNA
A;Residues: 1-65 <BRA>
A;Cross-references: GB:J04972; NID:g159478; PIDN:AAA29299.1; PID:g159479
C;Genetics:
A;Introns: #status absent
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-28/Product: adipokinetic hormone #status predicted <MAT>
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predic
F;28/Modified site: amidated carboxyl end (Gly) (amide in mature form from following

Query Match 85.0%; Score 17; DB 1; Length 65;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 23 FTSSW 27

RESULT 6
T12860
hypothetical protein yopZ - Bacillus subtilis phage SPBc2
C;Species: Bacillus subtilis phage SPBc2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C;Accession: T12860; H69918
R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 pro
A;Reference number: Z17583
A;Accession: T12860
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-67 <LAZ>
A;Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025574; PIDN:AAC13069.1
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H69918
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-67 <KUN>
A;Cross-references: GB:Z99114; GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB13989.1;
A;Experimental source: strain 168
C;Genetics:
A;Gene: yopZ

Query Match 85.0%; Score 17; DB 2; Length 67;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 49 FASSW 53

RESULT 7
A86942
hypothetical protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: A86942
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sc
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: A86942
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 <STO>
A;Cross-references: GB:AL450380; NID:g13092599; PIDN:CAC29773.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML0265

Query Match 85.0%; Score 17; DB 2; Length 70;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 14 FTTSW 18

RESULT 8
S15137
thioredoxin h2 - spinach (fragments)
C;Species: Spinacia oleracea (spinach)
C;Date: 25-Feb-1994 #sequence_revision 26-Jul-1996 #text_change 23-May-1997
C;Accession: S15137
R;Marcus, F.; Chamberlain, S.H.; Chu, C.; Masiarz, F.R.; Shin, S.; Yee, B.C.; Buchanan,
Arch. Biochem. Biophys. 287, 195-198, 1991
A;Title: Plant thioredoxin h: an animal-like thioredoxin occurring in multiple cell comp
A;Reference number: S15137; MUID:91378382; PMID:1897989
A;Accession: S15137
A;Molecule type: protein
A;Residues: 1-72 <MAR>
C;Superfamily: thioredoxin; thioredoxin homology
C;Keywords: redox-active disulfide

Query Match 85.0%; Score 17; DB 2; Length 72;
Best Local Similarity 40.0%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 6 FTASW 10

RESULT 9
S18581
pufQ protein - Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Sep-1998
C;Accession: S18581; S32854
R;Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.
Mol. Microbiol. 5, 2649-2661, 1991
A;Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg
A;Reference number: S18580; MUID:92140030; PMID:1779756
A;Accession: S18581
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 <HUN>
A;Cross-references: EMBL:X68795; NID:g49170; PID:g49175
C;Genetics:
A;Gene: pufQ
C;Superfamily: pufQ protein

Query Match 85.0%; Score 17; DB 2; Length 77;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 60 FASAW 64

RESULT 10
T50756
pufQ protein [imported] - Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C;Accession: T50756
R;Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroide
A;Reference number: Z25222; MUID:20115911; PMID:10648776
A;Accession: T50756
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-77 <CHO>
A;Cross-references: EMBL:AF195122; PIDN:AAF24300.1
A;Experimental source: strain 2.4.1
C;Genetics:
A;Gene: pufQ
C;Superfamily: pufQ protein

Query Match 85.0%; Score 17; DB 2; Length 77;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 60 FASAW 64

RESULT 11
E69268
hypothetical protein AF0149 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: E69268
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69268
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-84 <KLE>
A;Cross-references: GB:AE001096; GB:AE000782; NID:g2689419; PIDN:AAB91088.1; PID:g265

Query Match 85.0%; Score 17; DB 2; Length 84;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 42 FAAAW 46

RESULT 12
B46264
thioredoxin 2 - slime mold (Dictyostelium discoideum) (fragment)
C;Species: Dictyostelium discoideum
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 11-Jun-1999
C;Accession: B46264
R;Wetterauer, B.; Jacquot, J.P.; Veron, M.
J. Biol. Chem. 267, 9895-9904, 1992
A;Title: Thioredoxins from Dictyostelium discoideum are a developmentally regulated m

A;Reference number: A46264; MUID:92250653; PMID:1577820
A;Accession: B46264
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-88 <WET>
A;Cross-references: GB:M91382; NID:g167930; PIDN:AAA33259.1; PID:g167931
C;Superfamily: thioredoxin; thioredoxin homology
F;8-88/Domain: thioredoxin homology <THR>

Query Match 85.0%; Score 17; DB 2; Length 88;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 26 FSAAW 30

RESULT 13
F47624
Ig heavy chain V-I region - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: F47624
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation
A;Reference number: A47624; MUID:90237760; PMID:2110243
A;Accession: F47624
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-98 <HAI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 17; DB 2; Length 98;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 29 FSSTW 33

RESULT 14
S37447
gene E2 protein - human papillomavirus type 5 (fragment)
C;Species: human papillomavirus type 5
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C;Accession: S37447
R;Deau, A.C.
submitted to the EMBL Data Library, August 1993
A;Reference number: S37440
A;Accession: S37447
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <DEA>
A;Cross-references: EMBL:X74651; NID:g404204; PIDN:CAA52715.1; PID:g404205
C;Superfamily: papillomavirus E2 protein

Query Match 85.0%; Score 17; DB 2; Length 99;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 46 FSTTW 50

RESULT 15
S37448
gene E2 protein - human papillomavirus type 5 (fragment)
C;Species: human papillomavirus type 5
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Apr-1995
C;Accession: S37448
R;Deau, A.C.
submitted to the EMBL Data Library, August 1993
A;Reference number: S37440
A;Accession: S37448
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <DEA>
A;Cross-references: EMBL:X74652
C;Superfamily: papillomavirus E2 protein

Query Match 85.0%; Score 17; DB 2; Length 99;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 46 FSTTW 50

Search completed: January 29, 2003, 14:12:36
Job time : 16 secs

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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:07:27 ; Search time 11 Seconds
(without alignments)
18.853 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	38	1	PSAI_PROMA	Q87786 prochloroco
2	17	85.0	65	1	AKH_MANSE	P08901 manduca sex
3	17	85.0	77	1	PUFQ_RHOSH	P16069 rhodobacter
4	17	85.0	84	1	Y149_ARCFU	O30088 archaeoglob
5	17	85.0	88	1	THI2_DICDI	P29446 dictyosteli
6	17	85.0	93	1	CD06_HUMAN	Q99440 homo sapien
7	17	85.0	104	1	THIO_BOVIN	O97680 bos taurus
8	17	85.0	104	1	THIO_CALJA	Q9bdj3 callithrix
9	17	85.0	104	1	THIO_CHICK	P08629 gallus gall
10	17	85.0	104	1	THIO_HORSE	O97508 equus cabal
11	17	85.0	104	1	THIO_HUMAN	P10599 homo sapien
12	17	85.0	104	1	THIO_MACMU	P29451 macaca mula
13	17	85.0	104	1	THIO_MOUSE	P10639 mus musculu
14	17	85.0	104	1	THIO_OPHHA	Q98tx1 ophiophagus
15	17	85.0	104	1	THIO_PIG	P82460 sus scrofa
16	17	85.0	104	1	THIO_RABIT	P08628 oryctolagus
17	17	85.0	104	1	THIO_RAT	P11232 rattus norv
18	17	85.0	104	1	THIO_SHEEP	P50413 ovis aries
19	17	85.0	107	1	THIO_ICTPU	Q9dqi3 ictalurus p
20	17	85.0	112	1	THIH_CHLRE	P80028 chlamydomon
21	17	85.0	114	1	THH1_ARATH	P29448 arabidopsis
22	17	85.0	115	1	HV3S_HUMAN	P01780 homo sapien
23	17	85.0	116	1	THIH_FAGES	Q96419 fagopyrum e
24	17	85.0	118	1	THH2_TOBAC	Q07090 nicotiana t
25	17	85.0	118	1	THH3_ARATH	Q42403 arabidopsis
26	17	85.0	118	1	THH5_ARATH	Q39241 arabidopsis
27	17	85.0	118	1	THIH_RICCO	Q43636 ricinus com
28	17	85.0	119	1	THH2_BRANA	Q39362 brassica na
29	17	85.0	119	1	THH4_ARATH	Q39239 arabidopsis
30	17	85.0	122	1	THIH_ORYSA	Q42443 oryza sativ
31	17	85.0	125	1	THIH_PICMA	O65049 picea maria
32	17	85.0	126	1	THH1_TOBAC	P29449 nicotiana t
33	17	85.0	126	1	THIH_WHEAT	O64394 triticum ae
34	17	85.0	133	1	THH2_ARATH	Q38879 arabidopsis
35	17	85.0	141	1	YE17_YEAST	P40102 saccharomyc
36	17	85.0	174	1	YC21_PORPU	P51380 porphyra pu
37	17	85.0	182	1	FCPD_MACPY	Q40298 macrocystis
38	17	85.0	208	1	ENGB_HELPJ	Q9zj42 helicobacte
39	17	85.0	208	1	ENGB_HELPY	O26087 helicobacte
40	17	85.0	211	1	FCPF_MACPY	Q40300 macrocystis
41	17	85.0	212	1	HAG2_EIKCO	P35648 eikenella c
42	17	85.0	216	1	FCPC_MACPY	Q40299 macrocystis
43	17	85.0	232	1	HXB9_XENLA	P31272 xenopus lae
44	17	85.0	241	1	PGPB_HAEIN	P44570 haemophilus
45	17	85.0	251	1	GUNX_PRUPE	P38534 prunus pers

ALIGNMENTS

RESULT 1
PSAI_PROMA
ID PSAI_PROMA STANDARD; PRT; 38 AA.
AC O87786;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Photosystem I reaction center subunit VIII.
GN PSAI.
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SARG / CCMP 1375;
RA van der Staay G.W.M., Moon-Van Der Staay S.Y., Garczarek L.,
RA Partensky F.;
RT "Characterization of the photosystem I subunits PsaI and PsaL from two
RT strains of the marine oxyphototrophic.";
RL Photosyn. Res. 57:183-191(1998).
CC -!- FUNCTION: MAY HELP IN THE ORGANIZATION OF THE PSAL SUBUNIT.
CC -!- SIMILARITY: BELONGS TO THE PSAI FAMILY.
CC ---
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CC ---
DR EMBL; Z98594; CAB11178.1; ALT_INIT.
DR InterPro; IPR001302; PSI_8.
DR Pfam; PF00796; PSI_8; 1.
KW Photosystem I; Photosynthesis; Transmembrane.
FT TRANSMEM 12 32 POTENTIAL.
SQ SEQUENCE 38 AA; 4081 MW; 19DECDABA650A2F2 CRC64;

Query Match 85.0%; Score 17; DB 1; Length 38;
Best Local Similarity 40.0%; Pred. No. 4.6e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 5 FAATW 9

RESULT 2
AKH_MANSE
ID AKH_MANSE STANDARD; PRT; 65 AA.
AC P08901;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Adipokinetic hormone precursor (AKH).

```
OS   Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm), and
OS   Heliothis zea (Corn earworm) (Bollworm).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC   Ditrysia; Sphingiodea; Sphingidae; Sphinginae; Manduca.
OX   NCBI_TaxID=7130, 7113;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=M.sexta;
RX   MEDLINE=89327232; PubMed=2753887;
RA   Bradfield J.Y., Keeley L.L.;
RT   "Adipokinetic hormone gene sequence from Manduca sexta.";
RL   J. Biol. Chem. 264:12791-12793(1989).
RN   [2]
RP   SEQUENCE OF 20-28.
RC   SPECIES=M.sexta;
RX   MEDLINE=86077009; PubMed=4074373;
RA   Ziegler R., Eckart K., Schwarz H., Keller R.;
RT   "Amino acid sequence of Manduca sexta adipokinetic hormone elucidated
RT   by combined fast atom bombardment (FAB)/tandem mass spectrometry.";
RL   Biochem. Biophys. Res. Commun. 133:337-342(1985).
RN   [3]
RP   SEQUENCE OF 20-28.
RC   SPECIES=H.zea;
RX   MEDLINE=86186794; PubMed=3964263;
RA   Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Holman G.M.,
RA   Wagner R.M., Ridgway R.L., Hayes D.K.;
RT   "Isolation and primary structure of a peptide from the corpora
RT   cardiaca of Heliothis zea with adipokinetic activity.";
RL   Biochem. Biophys. Res. Commun. 135:622-628(1986).
CC   -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC       CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC       DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC       MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; J04972; AAA29299.1; -.
DR   PIR; A32613; A32613.
DR   PIR; A24244; A24244.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight; Cleavage on pair of basic residues;
KW   Signal.
FT   SIGNAL        1     19
FT   CHAIN        20     65       ADIPOKINETIC PROHORMONE.
FT   PEPTIDE      20     28       ADIPOKINETIC HORMONE.
FT   MOD_RES      20     20       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      28     28       AMIDATION (G-29 PROVIDE AMIDE GROUP).
SQ   SEQUENCE   65 AA;  7401 MW;  1812E58E6F2D7852 CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 65;
  Best Local Similarity   40.0%;  Pred. No. 6.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      23 FTSSW 27


RESULT 3
PUFQ_RHOSH
ID   PUFQ_RHOSH     STANDARD;      PRT;    77 AA.
AC   P16069;
DT   01-APR-1990 (Rel. 14, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
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DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Protein pufQ.
GN   PUFQ.
OS   Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC   Rhodobacter.
OX   NCBI_TaxID=1063;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NC13;
RX   MEDLINE=92140030; PubMed=1779756;
RA   Hunter C.N., McGlynn P., Ashby M.K., Burgess J.G., Olsen J.D.;
RT   "DNA sequencing and complementation/deletion analysis of the bchA-puf
RT   operon region of Rhodobacter sphaeroides: in vivo mapping of the
RT   oxygen-regulated puf promoter.";
RL   Mol. Microbiol. 5:2649-2661(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX   MEDLINE=94245622; PubMed=8188596;
RA   Gong L., Lee J.K., Kaplan S.;
RT   "The Q gene of Rhodobacter sphaeroides: its role in puf operon
RT   expression and spectral complex assembly.";
RL   J. Bacteriol. 176:2946-2961(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX   MEDLINE=20115911; PubMed=10648776;
RA   Choudhary M., Kaplan S.;
RT   "DNA sequence analysis of the photosynthesis region of Rhodobacter
RT   sphaeroides 2.4.1.";
RL   Nucleic Acids Res. 28:862-867(2000).
RN   [4]
RP   SEQUENCE OF 1-7 FROM N.A.
RX   MEDLINE=93173096; PubMed=8437569;
RA   McGlynn P., Hunter C.N.;
RT   "Genetic analysis of the bchC and bchA genes of Rhodobacter
RT   sphaeroides.";
RL   Mol. Gen. Genet. 236:227-234(1993).
RN   [5]
RP   SEQUENCE OF 44-77 FROM N.A.
RX   MEDLINE=87109067; PubMed=3027044;
RA   Kiley P.J., Donohue T.J., Havelka W.A., Kaplan S.;
RT   "DNA sequence and in vitro expression of the B875 light-harvesting
RT   polypeptides of Rhodobacter sphaeroides.";
RL   J. Bacteriol. 169:742-750(1987).
CC   -!- FUNCTION: REQUIRED FOR BACTERIOCHLOROPHYLL BIOSYNTHESIS. DIRECTLY
CC       INVOLVED IN THE ASSEMBLY OF BOTH THE B875 AND B800-850 PIGMENT-
CC       PROTEIN COMPLEXES.
CC   -!- SIMILARITY: BELONGS TO THE PUFQ FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ010302; CAB38750.1; -.
DR   EMBL; L25894; AAD15241.1; -.
DR   EMBL; AF195122; AAF24300.1; -.
DR   EMBL; M15105; -; NOT_ANNOTATED_CDS.
DR   PIR; S18581; S18581.
KW   Photosynthesis; Chlorophyll biosynthesis.
FT   CONFLICT     36     36       A -> G (IN REF. 1).
SQ   SEQUENCE   77 AA;  8656 MW;  61127EF670B39EB6 CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 77;
  Best Local Similarity   40.0%;  Pred. No. 7.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
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          |   |
Db      60 FASAW 64


RESULT 4
Y149_ARCFU
ID   Y149_ARCFU     STANDARD;      PRT;    84 AA.
AC   O30088;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein AF0149.
GN   AF0149.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC   Archaeoglobaceae; Archaeoglobus.
OX   NCBI_TaxID=2234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE=98049343; PubMed=9389475;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulphate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   ---------------------------------------------------------------------
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE001096; AAB91088.1; -.
DR   TIGR; AF0149; -.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM      4     20       POTENTIAL.
FT   TRANSMEM     27     49       POTENTIAL.
FT   TRANSMEM     59     81       POTENTIAL.
SQ   SEQUENCE   84 AA;  8893 MW;  E2FDF1FC6FFBF1EE CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 84;
  Best Local Similarity   40.0%;  Pred. No. 8.4e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      42 FAAAW 46


RESULT 5
THI2_DICDI
ID   THI2_DICDI     STANDARD;      PRT;    88 AA.
AC   P29446;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Thioredoxin 2 (Fragment).
GN   TRXB OR TRX2.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92250653; PubMed=1577820;
RA   Wetterauer B., Jacquot J.-P., Veron M.;
RT   "Thioredoxins from Dictyostelium discoideum are a developmentally
RT   regulated multigene family.";
RL   J. Biol. Chem. 267:9895-9904(1992).
CC   -!- FUNCTION: Participates in various redox reactions through the
CC       reversible oxidation of its active center dithiol to a disulfide
CC       and catalyzes dithiol-disulfide exchange reactions.
CC   ---------------------------------------------------------------------
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M91382; AAA33259.1; -.
DR   PIR; B46264; B46264.
DR   HSSP; P10599; 1ERV.
DR   DictyDb; DD05030; trxB.
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox-active center; Electron transport; Multigene family.
FT   DISULFID     31     34       REDOX-ACTIVE (BY SIMILARITY).
FT   NON_TER      88     88
SQ   SEQUENCE   88 AA;  10102 MW;  CEC73BCEFACB607C CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 88;
  Best Local Similarity   40.0%;  Pred. No. 8.7e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      26 FSAAW 30


RESULT 6
CD06_HUMAN
ID   CD06_HUMAN     STANDARD;      PRT;    93 AA.
AC   Q99440;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein C4orf6 (AC1 protein).
GN   C4ORF6 OR AC1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97169148; PubMed=9016955;
RA   Kito K., Ito T., Sakaki Y.;
RT   "Fluorescent differential display analysis of gene expression in
RT   differentiating neuroblastoma cells.";
RL   Gene 184:73-81(1997).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEUROBLASTOMA.
CC   ---------------------------------------------------------------------
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D82070; BAA11534.1; -.
DR   Genew; HGNC:13716; C4orf6.
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SQ   SEQUENCE   93 AA;  10499 MW;  A8786AC4A9990215 CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 93;
  Best Local Similarity   40.0%;  Pred. No. 9.1e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db     69 FAASW 73


RESULT 7
THIO_BOVIN
ID   THIO_BOVIN     STANDARD;      PRT;   104 AA.
AC   O97680;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Thioredoxin.
GN   TXN.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20189621; PubMed=10727087;
RA   Terashima H., Gotoh S., Yagi K., Mizoguchi T.;
RT   "cDNA sequence of bovine thioredoxin.";
RL   DNA Seq. 10:331-333(1999).
CC   -!- FUNCTION: Participates in various redox reactions through the
CC       reversible oxidation of its active center dithiol to a disulfide
CC       and catalyzes dithiol-disulfide exchange reactions (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AF104105; AAC83380.1; -.
DR   HSSP; P10599; 1ERT.
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PRINTS; PR00421; THIOREDOXIN.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox-active center; Electron transport.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   DISULFID     31     34       REDOX-ACTIVE (BY SIMILARITY).
SQ   SEQUENCE   104 AA;  11681 MW;  506CFF9696A2208D CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 104;
  Best Local Similarity   40.0%;  Pred. No. 9.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db     26 FSATW 30


RESULT 8
THIO_CALJA
ID   THIO_CALJA     STANDARD;      PRT;   104 AA.
AC   Q9BDJ3;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Thioredoxin.
GN   TXN OR TRX.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC   Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21576430; PubMed=11719593;
RA   Lopata A., Sibson M.C., Enders A.C., Bloomfield K.L., Gregory M.S.,
RA   Trapani G.D., Perkins A.V., Tonissen K.F., Clarke F.M.;
RT   "Expression and localization of thioredoxin during early implantation
RT   in the marmoset monkey.";
RL   Mol. Hum. Reprod. 7:1159-1165(2001).
CC   -!- FUNCTION: Participates in various redox reactions through the
CC       reversible oxidation of its active center dithiol to a disulfide
CC       and catalyzes dithiol-disulfide exchange reactions.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF353204; AAK30295.1; -.
DR   HSSP; P10599; 1ERT.
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PRINTS; PR00421; THIOREDOXIN.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox-active center; Electron transport.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   DISULFID     31     34       REDOX-ACTIVE (BY SIMILARITY).
SQ   SEQUENCE   104 AA;  11626 MW;  3E0F5243A04B8E81 CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 104;
  Best Local Similarity   40.0%;  Pred. No. 9.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db     26 FSATW 30


RESULT 9
THIO_CHICK
ID   THIO_CHICK     STANDARD;      PRT;   104 AA.
AC   P08629;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Thioredoxin.
GN   TXN.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88257080; PubMed=2838473;
RA   Jones S.W., Luk K.-C.;
RT   "Isolation of a chicken thioredoxin cDNA clone. Thioredoxin mRNA is
RT   differentially expressed in normal and Rous sarcoma virus-transformed
RT   chicken embryo fibroblasts.";
RL   J. Biol. Chem. 263:9607-9611(1988).
CC   -!- FUNCTION: Participates in various redox reactions through the
CC       reversible oxidation of its active center dithiol to a disulfide
```

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CC       and catalyzes dithiol-disulfide exchange reactions (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J03882; AAA49092.1; -.
DR   PIR; A30006; A30006.
DR   HSSP; P10599; 1ERT.
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PRINTS; PR00421; THIOREDOXIN.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox-active center; Electron transport.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   DISULFID     31     34       REDOX-ACTIVE (BY SIMILARITY).
SQ   SEQUENCE   104 AA;  11569 MW;  60B66B759010BB12 CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 104;
  Best Local Similarity   40.0%;  Pred. No. 9.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      26 FSATW 30


RESULT 10
THIO_HORSE
ID   THIO_HORSE     STANDARD;      PRT;   104 AA.
AC   O97508;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Thioredoxin.
GN   TXN.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Thoroughbred;
RA   Tajima Y., Ishida N.;
RT   "Molecular cloning of equine thioredoxin.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Participates in various redox reactions through the
CC       reversible oxidation of its active center dithiol to a disulfide
CC       and catalyzes dithiol-disulfide exchange reactions.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB022431; BAA37154.1; -.
DR   HSSP; P10599; 1ERV.
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PRINTS; PR00421; THIOREDOXIN.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox-active center; Electron transport.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   DISULFID     31     34       REDOX-ACTIVE (BY SIMILARITY).
SQ   SEQUENCE   104 AA;  11605 MW;  5E6C1092964C206D CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 104;
  Best Local Similarity   40.0%;  Pred. No. 9.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      26 FSATW 30


RESULT 11
THIO_HUMAN
ID   THIO_HUMAN     STANDARD;      PRT;   104 AA.
AC   P10599; Q96KI3;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Thioredoxin (ATL-derived factor) (ADF) (Surface associated sulphydryl
DE   protein) (SASP).
GN   TXN OR TRDX OR TRX OR TRX1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91340156; PubMed=1874447;
RA   Tonissen K.F., Wells J.R.E.;
RT   "Isolation and characterization of human thioredoxin-encoding genes.";
RL   Gene 102:221-228(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89008454; PubMed=3170595;
RA   Wollman E.E., D'Auriol L., Rimsky L., Shaw A., Jacquot J.-P.,
RA   Wingfield P., Graber P., Dessarps F.;
RT   "Cloning and expression of a cDNA for human thioredoxin.";
RL   J. Biol. Chem. 263:15506-15512(1988).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89251607; PubMed=2785919;
RA   Tagaya Y., Maeda Y., Mitsui A., Kndo N., Matsui H., Hamuro J.,
RA   Brown N., Arai K.-I., Yokota T., Wakasugi H., Yodoi J.;
RT   "ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to
RT   thioredoxin; possible involvement of dithiol-reduction in the IL-2
RT   receptor induction.";
RL   EMBO J. 8:757-764(1989).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lens;
RA   Reddy P.G., Bhuyan D.K., Bhuyan K.C.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lens;
RA   Liu A., Lou M.F.;
RT   "Cloning, purification and characterization of human lens
RT   thioredoxin.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Xu J.Y., Xu L., Li K.S., Dai R.;
RT   "Cloning and sequencing of thioredoxin cDNA from human brain.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cervix;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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RN   [8]
RP   SEQUENCE OF 1-14.
RX   MEDLINE=91151337; PubMed=1998498;
RA   Martin H., Dean M.;
RT   "Identification of a thioredoxin-related protein associated with
RT   plasma membranes.";
RL   Biochem. Biophys. Res. Commun. 175:123-128(1991).
RN   [9]
RP   STRUCTURE BY NMR.
RX   MEDLINE=90057393; PubMed=2684271;
RA   Forman-Kay J.D., Clore G.M., Dricoll P.C., Wingfield P.,
RA   Richards F.M., Gronenborn A.M.;
RT   "A proton nuclear magnetic resonance assignment and secondary
RT   structure determination of recombinant human thioredoxin.";
RL   Biochemistry 28:7088-7097(1989).
RN   [10]
RP   STRUCTURE BY NMR.
RX   MEDLINE=91159399; PubMed=2001356;
RA   Forman-Kay J.D., Clore G.M., Wingfield P., Gronenborn A.M.;
RT   "High-resolution three-dimensional structure of reduced recombinant
RT   human thioredoxin in solution.";
RL   Biochemistry 30:2685-2698(1991).
RN   [11]
RP   STRUCTURE BY NMR.
RX   MEDLINE=95006318; PubMed=7922028;
RA   Qin J., Clore G.M., Gronenborn A.M.;
RT   "The high-resolution three-dimensional solution structures of the
RT   oxidized and reduced states of human thioredoxin.";
RL   Structure 2:503-522(1994).
RN   [12]
RP   STRUCTURE BY NMR.
RX   MEDLINE=96347359; PubMed=8736558;
RA   Qin J., Clore G.M., Kennedy W.P., Kuszewski J., Gronenborn A.M.;
RT   "The solution structure of human thioredoxin complexed with its
RT   target from Ref-1 reveals peptide chain reversal.";
RL   Structure 4:613-620(1996).
RN   [13]
RP   X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RX   MEDLINE=96399719; PubMed=8805557;
RA   Weichsel A., Gasdaska J.R., Powis G., Montfort W.R.;
RT   "Crystal structures of reduced, oxidized, and mutated human
RT   thioredoxins: evidence for a regulatory homodimer.";
RL   Structure 4:735-751(1996).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF MUTANT ASN-60.
RX   MEDLINE=98039128; PubMed=9369469;
RA   Andersen J.F., Sanders D.A., Gasdaska J.R., Weichsel A., Powis G.,
RA   Montfort W.R.;
RT   "Human thioredoxin homodimers: regulation by pH, role of aspartate
RT   60, and crystal structure of the aspartate 60 --> asparagine
RT   mutant.";
RL   Biochemistry 36:13979-13988(1997).
RN   [15]
RP   ACTIVITY.
RX   MEDLINE=91097576; PubMed=2176490;
RA   Jacquot J.-P., de Lamotte F., Fontecav M., Schuermann P.,
RA   Decottignies P., Miginiac-Maslow M., Wollman E.;
RT   "Human thioredoxin reactivity-structure/function relationship.";
RL   Biochem. Biophys. Res. Commun. 173:1375-1381(1990).
CC   -!- FUNCTION: Participates in various redox reactions through the
CC       reversible oxidation of its active center dithiol to a disulfide
CC       and catalyzes dithiol-disulfide exchange reactions.
CC   -!- FUNCTION: ADF AUGMENTS THE EXPRESSION OF THE INTERLEUKIN-2
CC       RECEPTOR TAC (IL2R/P55).
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; X77584; CAA54687.1; -.
DR   EMBL; X54539; CAA38410.1; -.
DR   EMBL; X54540; CAA38410.1; JOINED.
DR   EMBL; X54541; CAA38410.1; JOINED.
DR   EMBL; J04026; AAA74596.1; -.
DR   EMBL; AF276919; AAF86466.1; -.
DR   EMBL; AY004872; AAF87085.1; -.
DR   EMBL; AF313911; AAG34699.1; -.
DR   EMBL; BC003377; AAH03377.1; -.
DR   PIR; A31993; A31993.
DR   PIR; S04106; S04106.
DR   PIR; JH0568; JH0568.
DR   PDB; 3TRX; 15-JAN-93.
DR   PDB; 4TRX; 15-JAN-93.
DR   PDB; 1TRS; 30-SEP-94.
DR   PDB; 1TRU; 30-SEP-94.
DR   PDB; 1TRV; 30-SEP-94.
DR   PDB; 1TRW; 30-SEP-94.
DR   PDB; 1AIU; 07-JUL-97.
DR   PDB; 1ERT; 14-OCT-96.
DR   PDB; 1ERU; 01-AUG-96.
DR   PDB; 1ERV; 14-OCT-96.
DR   PDB; 1ERW; 14-OCT-96.
DR   PDB; 1CQG; 01-AUG-96.
DR   PDB; 1CQH; 01-AUG-96.
DR   PDB; 1MDI; 03-JUN-95.
DR   PDB; 1MDJ; 20-JUL-95.
DR   PDB; 1MDK; 20-JUL-95.
DR   PDB; 1AUC; 25-FEB-98.
DR   SWISS-2DPAGE; P10599; HUMAN.
DR   Aarhus/Ghent-2DPAGE; 8006; IEF.
DR   PHCI-2DPAGE; P10599; -.
DR   Siena-2DPAGE; P10599; -.
DR   Genew; HGNC:12435; TXN.
DR   MIM; 187700; -.
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PRINTS; PR00421; THIOREDOXIN.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox-active center; Electron transport; 3D-structure.
FT   INIT_MET      0      0
FT   DISULFID     31     34       REDOX-ACTIVE.
FT   DISULFID     72     72       INTERCHAIN.
FT   CONFLICT     38     38       K -> N (IN REF. 2 AND 4).
FT   CONFLICT     73     73       M -> T (IN REF. 2 AND 4).
FT   STRAND        2      3
FT   HELIX         7     16
FT   TURN         18     19
FT   STRAND       22     27
FT   HELIX        32     35
FT   TURN         36     37
FT   HELIX        38     41
FT   TURN         42     43
FT   HELIX        44     47
FT   STRAND       52     57
FT   TURN         58     60
FT   HELIX        62     68
FT   TURN         69     69
FT   STRAND       75     80
FT   TURN         81     82
FT   STRAND       83     89
FT   HELIX        94    103
SQ   SEQUENCE   104 AA;  11606 MW;  7FFABDF3B6EBE33A CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 104;
  Best Local Similarity   40.0%;  Pred. No. 9.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
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Db      26 FSATW 30


RESULT 12
THIO_MACMU
ID   THIO_MACMU     STANDARD;      PRT;   104 AA.
AC   P29451;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Thioredoxin.
GN   TXN.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92181438; PubMed=1543487;
RA   An G., Wu R.;
RT   "Thioredoxin gene expression is transcriptionally up-regulated by
RT   retinol in monkey conducting airway epithelial cells.";
RL   Biochem. Biophys. Res. Commun. 183:170-175(1992).
CC   -!- FUNCTION: Participates in various redox reactions through the
CC       reversible oxidation of its active center dithiol to a disulfide
CC       and catalyzes dithiol-disulfide exchange reactions.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M84643; AAA36921.1; -.
DR   PIR; JS0667; JS0667.
DR   HSSP; P10599; 1ERT.
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PRINTS; PR00421; THIOREDOXIN.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox-active center; Electron transport.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   DISULFID     31     34       REDOX-ACTIVE (BY SIMILARITY).
SQ   SEQUENCE   104 AA;  11606 MW;  C804D5152F8870EB CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 104;
  Best Local Similarity   40.0%;  Pred. No. 9.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      26 FSATW 30


RESULT 13
THIO_MOUSE
ID   THIO_MOUSE     STANDARD;      PRT;   104 AA.
AC   P10639; Q9D8R0;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Thioredoxin (ATL-derived factor) (ADF).
GN   TXN OR TXN1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89251607; PubMed=2785919;
RA   Tagaya Y., Maeda Y., Mitsui A., Kndo N., Matsui H., Hamuro J.,
RA   Brown N., Arai K.-I., Yokota T., Wakasugi H., Yodoi J.;
RT   "ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to
RT   thioredoxin; possible involvement of dithiol-reduction in the IL-2
RT   receptor induction.";
RL   EMBO J. 8:757-764(1989).
RN   [2]
RP   REVISIONS.
RX   MEDLINE=94244626; PubMed=8187776;
RA   Tagaya Y., Maeda Y., Mitsui A., Kndo N., Matsui H., Hamuro J.,
RA   Brown N., Arai K.-I., Yokota T., Wakasugi H., Yodoi J.;
RL   EMBO J. 13:2244-2244(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv; TISSUE=Liver;
RX   MEDLINE=95137382; PubMed=7835695;
RA   Matsui M., Taniguchi Y., Hirota K., Taketo M., Yodoi J.;
RT   "Structure of the mouse thioredoxin-encoding gene and its processed
RT   pseudogene.";
RL   Gene 152:165-171(1995).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Participates in various redox reactions through the
CC       reversible oxidation of its active center dithiol to a disulfide
CC       and catalyzes dithiol-disulfide exchange reactions.
CC   -!- FUNCTION: ADF AUGMENTS THE EXPRESSION OF THE INTERLEUKIN-2
CC       RECEPTOR TAC (IL2R/P55).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X77585; CAA54688.1; -.
DR   EMBL; D21859; BAA04881.1; -.
DR   EMBL; D21855; BAA04881.1; JOINED.
DR   EMBL; D21856; BAA04881.1; JOINED.
DR   EMBL; D21857; BAA04881.1; JOINED.
DR   EMBL; D21858; BAA04881.1; JOINED.
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DR   EMBL; AK007537; BAB25096.1; -.
DR   EMBL; AK007790; BAB25256.1; -.
DR   EMBL; BC010756; AAH10756.1; -.
DR   PIR; S04107; S04107.
DR   HSSP; P10599; 1ERT.
DR   SWISS-2DPAGE; P10639; MOUSE.
DR   MGD; MGI:98874; Txnl.
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PRINTS; PR00421; THIOREDOXIN.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox-active center; Electron transport.
FT   INIT_MET      0      0
FT   DISULFID     31     34       REDOX-ACTIVE (BY SIMILARITY).
FT   CONFLICT     99     99       S -> C (IN REF. 4; BAB25256).
SQ   SEQUENCE   104 AA;  11544 MW;  60BE6196090AC773 CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 104;
  Best Local Similarity   40.0%;  Pred. No. 9.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      26 FSATW 30


RESULT 14
THIO_OPHHA
ID   THIO_OPHHA      STANDARD;      PRT;   104 AA.
AC   Q98TX1;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Thioredoxin.
GN   TXN.
OS   Ophiophagus hannah (King cobra) (Naja hannah).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Elapidae; Elapinae; Ophiophagus.
OX   NCBI_TaxID=8665;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Lee W., Liu H., Zhang Y.;
RT   "cDNA sequence of Ophiophagus hannah venom gland thioredoxin
RT   protein.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Participates in various redox reactions through the
CC       reversible oxidation of its active center dithiol to a disulfide
CC       and catalyzes dithiol-disulfide exchange reactions (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF321769; AAK09384.1; -.
DR   HSSP; P10599; 1ERT.
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PRINTS; PR00421; THIOREDOXIN.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox-active center; Electron transport.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   DISULFID     31     34       REDOX-ACTIVE (BY SIMILARITY).
SQ   SEQUENCE   104 AA;  11872 MW;  852B96C8EF850AFB CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 104;
  Best Local Similarity   40.0%;  Pred. No. 9.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      26 FSATW 30


RESULT 15
THIO_PIG
ID   THIO_PIG       STANDARD;      PRT;   104 AA.
AC   P82460; Q95JF9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Thioredoxin.
GN   TXN.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Yu G.W., Xu J.Y., Xu L., Cheung P.Y., Lee K.S.;
RT   "The cloning and expression of porcine thioredoxin in E. coli.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-33.
RC   TISSUE=Erythrocyte;
RA   Lee K.S., Tang W.K., Cheung P.Y., Siu Y.L., Wong N.S.;
RL   Submitted (MAY-2000) to the SWISS-PROT data bank.
CC   -!- FUNCTION: Participates in various redox reactions through the
CC       reversible oxidation of its active center dithiol to a disulfide
CC       and catalyzes dithiol-disulfide exchange reactions.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- TISSUE SPECIFICITY: ERYTHROCYTE.
CC   -!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF382821; AAK60272.1; -.
DR   HSSP; P10599; 1ERV.
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox-active center; Electron transport.
FT   INIT_MET      0      0
FT   DISULFID     31     34       REDOX-ACTIVE (BY SIMILARITY).
SQ   SEQUENCE   104 AA;  11697 MW;  9B16FF9696A2396A CRC64;

  Query Match             85.0%;  Score 17;  DB 1;  Length 104;
  Best Local Similarity   40.0%;  Pred. No. 9.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      26 FSATW 30


Search completed: January 29, 2003, 14:11:37
Job time : 11 secs
```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:09:57 ; Search time 29 Seconds
(without alignments)
35.525 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	13	8	Q9XLI2	Q9xli2 bemisia tab
2	17	85.0	26	10	Q9S880	Q9s880 spinacia ol
3	17	85.0	32	2	O05602	O05602 pseudomonas
4	17	85.0	36	13	Q9PV61	Q9pv61 mola mola (
5	17	85.0	38	13	Q9PV63	Q9pv63 pseudopleur
6	17	85.0	40	13	Q9PV89	Q9pv89 triakis sp.
7	17	85.0	40	13	Q9PV88	Q9pv88 torpedo cal
8	17	85.0	40	13	Q9PV85	Q9pv85 osteoglossu
9	17	85.0	40	13	Q9PV84	Q9pv84 anguilla sp
10	17	85.0	40	13	Q9PV82	Q9pv82 barbus tetr
11	17	85.0	40	13	Q9PV81	Q9pv81 esox lucius
12	17	85.0	40	13	Q9PV80	Q9pv80 plecoglossu
13	17	85.0	40	13	Q9PT24	Q9pt24 oncorhynchu
14	17	85.0	40	13	Q9PV79	Q9pv79 galaxias ma
15	17	85.0	40	13	Q9PU06	Q9pu06 lampris sp.
16	17	85.0	40	13	Q9PV78	Q9pv78 lophius sp.
17	17	85.0	40	13	Q9PV77	Q9pv77 mugil cepha
18	17	85.0	40	13	Q9PU05	Q9pu05 hemiramphus
19	17	85.0	40	13	Q9PU04	Q9pu04 fundulus he
20	17	85.0	40	13	Q9PV75	Q9pv75 poecilia la
21	17	85.0	40	13	Q9PU03	Q9pu03 sargocentro
22	17	85.0	40	13	Q9PU02	Q9pu02 zeus faber
23	17	85.0	40	13	Q9PV74	Q9pv74 hippocampus
24	17	85.0	40	13	Q9PV73	Q9pv73 mastacembel
25	17	85.0	40	13	Q9PU01	Q9pu01 dendrochiru
26	17	85.0	40	13	Q9PV72	Q9pv72 lates calca
27	17	85.0	40	13	Q9PU00	Q9pu00 dicentrarch
28	17	85.0	40	13	Q9PTZ9	Q9ptz9 epinephelus
29	17	85.0	40	13	Q9PV71	Q9pv71 mullus sp.
30	17	85.0	40	13	Q9PV70	Q9pv70 dissostichu
31	17	85.0	40	13	Q9PTZ8	Q9ptz8 salarias sp
32	17	85.0	40	13	Q9PV69	Q9pv69 cryptocentr
33	17	85.0	40	13	Q9PV68	Q9pv68 acanthurus
34	17	85.0	40	13	Q9PV66	Q9pv66 stromateus
35	17	85.0	40	13	Q9PV65	Q9pv65 colisa lali
36	17	85.0	40	13	Q9PV64	Q9pv64 channa sp.
37	17	85.0	40	13	Q9PV62	Q9pv62 ostracion s
38	17	85.0	41	13	Q9PUU2	Q9puu2 polypterus
39	17	85.0	44	16	Q8XPJ4	Q8xpj4 ralstonia s
40	17	85.0	53	9	O80077	O80077 staphylococ
41	17	85.0	53	9	Q9B0G7	Q9b0g7 staphylococ
42	17	85.0	53	9	Q9G031	Q9g031 bacteriopha
43	17	85.0	53	9	Q8SDM7	Q8sdm7 staphylococ
44	17	85.0	53	16	Q99SQ2	Q99sq2 staphylococ
45	17	85.0	53	16	Q931J8	Q931j8 staphylococ

ALIGNMENTS

RESULT 1
Q9XLI2
ID Q9XLI2 PRELIMINARY; PRT; 13 AA.
AC Q9XLI2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome oxidase I (Fragment).
OS Bemisia tabaci (Sweetpotato whitefly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
OC Aleyrodiformes; Aleyrodoidea; Aleyrodidae; Aleyrodinae; Bemisia.
OX NCBI_TaxID=7038;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10583831;
RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,
RA Brown J.K.;
RT "A phylogeographical analysis of the Bemisia tabaci species complex
RT based on mitochondrial DNA markers.";
RL Mol. Ecol. 8:1683-1691(1999).
DR EMBL; AF110703; AAD28415.1; -.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;

Query Match 85.0%; Score 17; DB 8; Length 13;
Best Local Similarity 40.0%; Pred. No. 8.2e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1 FXXXW 5
           |   |
Db       3 FTSSW 7
```

RESULT 2
Q9S880
ID Q9S880 PRELIMINARY; PRT; 26 AA.

```
AC   Q9S880;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Thioredoxin H2 (Fragment).
OS   Spinacia oleracea (Spinach).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX   NCBI_TaxID=3562;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=91378382; PubMed=1897989;
RA   Marcus F., Chamberlain S.H., Chu C., Masiarz F.R., Shin S., Yee B.C.,
RA   Buchanan B.B.;
RT   "Plant thioredoxin h: an animal-like thioredoxin occurring in multiple
RT   cell compartments.";
RL   Arch. Biochem. Biophys. 287:195-198(1991).
DR   InterPro; IPR000063; Thiored.
DR   Pfam; PF00085; thiored; 1.
DR   PROSITE; PS00194; THIOREDOXIN; 1.
KW   Redox-active center.
FT   NON_TER       1      1
FT   NON_TER      26     26
SQ   SEQUENCE   26 AA;  2880 MW;  A5317FC47DDB8863 CRC64;

  Query Match             85.0%;  Score 17;  DB 10;  Length 26;
  Best Local Similarity   40.0%;  Pred. No. 1.5e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       6 FTASW 10


RESULT 3
O05602
ID   O05602      PRELIMINARY;      PRT;    32 AA.
AC   O05602;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Transposon Tn5041 DNA (Fragment).
OS   Pseudomonas sp.
OC   Bacteria; Proteobacteria.
OX   NCBI_TaxID=306;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=KHP41; TRANSPOSON=TN5041;
RX   MEDLINE=97419493; PubMed=9274008;
RA   Khloldii G.Y., Yurieva O.V., Gorlenko Z.M., Mindlin S.Z., Bass I.A.,
RA   Lomovskaya O.L., Kopteva A.V., Nikiforov V.G.;
RT   "Tn5041 : a chimeric mercury resistance transposon closely related to
RT   the toluene degradative transposon Tn4651.";
RL   Microbiology 143:2549-2556(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=KHP41; TRANSPOSON=TN5041;
RA   Kholodii G.Y., Mindlin S.Z., Gorlenko Z.M., Bass I.A., Kalyaeva E.S.,
RA   Nikiforov V.;
RT   "Host-dependent transposition of Tn5041.";
RL   Russ. J. Genet. 36:365-373(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=KHP41; TRANSPOSON=TN5041;
RA   Kholodii G.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X98999; CAA67458.1; -.
FT   NON_TER       1      1
FT   NON_TER      32     32
SQ   SEQUENCE   32 AA;  3298 MW;  AF42B5EEF917077A CRC64;

  Query Match             85.0%;  Score 17;  DB 2;  Length 32;
  Best Local Similarity   40.0%;  Pred. No. 1.7e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      11 FSSSW 15


RESULT 4
Q9PV61
ID   Q9PV61      PRELIMINARY;      PRT;    36 AA.
AC   Q9PV61;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Mola mola (ocean sunfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Molidae; Mola.
OX   NCBI_TaxID=94237;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6SUNFISH;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137130; AAD54215.1; -.
DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      36     36
SQ   SEQUENCE   36 AA;  4181 MW;  DE01642A8CAAFC18 CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 36;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      32 FSSSW 36


RESULT 5
Q9PV63
ID   Q9PV63      PRELIMINARY;      PRT;    38 AA.
AC   Q9PV63;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
OS   americanus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
OX   NCBI_TaxID=8265;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6FLOUNDER;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137128; AAD54213.1; -.
```

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DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      38     38
SQ   SEQUENCE   38 AA;  4424 MW;  41C67E01642A8CB0 CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 38;
  Best Local Similarity   40.0%;  Pred. No. 2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db     32 FSSSW 36


RESULT 6
Q9PV89
ID   Q9PV89      PRELIMINARY;      PRT;    40 AA.
AC   Q9PV89;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Triakis sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC   Triakis.
OX   NCBI_TaxID=94228;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6SHARK;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137083; AAD54177.1; -.
DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      40     40
SQ   SEQUENCE   40 AA;  4604 MW;  796B35B9D1EB5569 CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 40;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db     32 FTSSW 36


RESULT 7
Q9PV88
ID   Q9PV88      PRELIMINARY;      PRT;    40 AA.
AC   Q9PV88;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Torpedo californica (Pacific electric ray).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC   Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX   NCBI_TaxID=7787;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6TORP;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137084; AAD54178.1; -.
DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
DR   PROSITE; PS50021; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      40     40
SQ   SEQUENCE   40 AA;  4595 MW;  5E9B2565075B5576 CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 40;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db     32 FTSSW 36


RESULT 8
Q9PV85
ID   Q9PV85      PRELIMINARY;      PRT;    40 AA.
AC   Q9PV85;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Osteoglossum sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC   Osteoglossiformes; Osteoglossidae; Osteoglossum.
OX   NCBI_TaxID=27725;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6DRAGONFISH;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137087; AAD54181.1; -.
DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      40     40
SQ   SEQUENCE   40 AA;  4598 MW;  B48648166BDB57E5 CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 40;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db     32 FSSSW 36


RESULT 9
Q9PV84
ID   Q9PV84      PRELIMINARY;      PRT;    40 AA.
AC   Q9PV84;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Anguilla sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
```

```
CC   Anguilla.
CX   NCBI_TaxID=62126;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6EEL;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137088; AAD54182.1; -.
DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
DR   PROSITE; PS50021; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      40     40
SQ   SEQUENCE   40 AA;  4574 MW;  557846E66BDB5437 CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 40;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      32 FSSSW 36


RESULT 10
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ID   Q9PV82       PRELIMINARY;      PRT;    40 AA.
AC   Q9PV82;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Barbus tetrazona.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Barbus.
OX   NCBI_TaxID=94221;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6TIGERBARB;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137090; AAD54184.1; -.
DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      40     40
SQ   SEQUENCE   40 AA;  4573 MW;  459B37C19BC3E736 CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 40;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      32 FSSSW 36


RESULT 11
Q9PV81
ID   Q9PV81       PRELIMINARY;      PRT;    40 AA.
AC   Q9PV81;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Esox lucius (Northern pike).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Esociformes;
OC   Esocidae; Esox.
OX   NCBI_TaxID=8010;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6PIKE;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137091; AAD54185.1; -.
DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      40     40
SQ   SEQUENCE   40 AA;  4542 MW;  09165AA193794B14 CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 40;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      32 FSSSW 36


RESULT 12
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ID   Q9PV80       PRELIMINARY;      PRT;    40 AA.
AC   Q9PV80;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Plecoglossus altivelis.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Osmeridae; Plecoglossus.
OX   NCBI_TaxID=61084;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6AYU;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137092; AAD54186.1; -.
DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      40     40
SQ   SEQUENCE   40 AA;  4512 MW;  B4931BF59BDB542A CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 40;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      32 FSSSW 36


RESULT 13
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Q9PT24
ID   Q9PT24      PRELIMINARY;      PRT;    40 AA.
AC   Q9PT24;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6TROUT;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137093; AAD54187.1; -.
DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      40     40
SQ   SEQUENCE   40 AA;  4551 MW;  B4865AA19BDB4B17 CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 40;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      32 FSSSW 36


RESULT 14
Q9PV79
ID   Q9PV79      PRELIMINARY;      PRT;    40 AA.
AC   Q9PV79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Galaxias maculatus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Galaxiidae; Galaxias.
OX   NCBI_TaxID=61620;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6GAL;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137094; AAD54188.1; -.
DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      40     40
SQ   SEQUENCE   40 AA;  4613 MW;  BA7C92D67E01642A CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 40;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      32 FSSSW 36


RESULT 15
Q9PU06
ID   Q9PU06      PRELIMINARY;      PRT;    40 AA.
AC   Q9PU06;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Dystrophin (Fragment).
GN   DYST.
OS   Lampris sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Lampridiformes; Lamprididae; Lampris.
OX   NCBI_TaxID=94303;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DYST6LAMP;
RX   MEDLINE=99398697; PubMed=10468597;
RA   Venkatesh B., Ning Y., Brenner S.;
RT   "Late changes in spliceosomal introns define clades in vertebrate
RT   evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR   EMBL; AF137096; AAD54189.1; -.
DR   EMBL; AF137095; AAD54189.1; JOINED.
DR   HSSP; P46939; 1BHD.
DR   InterPro; IPR001715; Calponin-like.
DR   Pfam; PF00307; CH; 1.
FT   NON_TER       1      1
FT   NON_TER      40     40
SQ   SEQUENCE   40 AA;  4610 MW;  B49D49A67E01642A CRC64;

  Query Match             85.0%;  Score 17;  DB 13;  Length 40;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      32 FSSSW 36


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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:07:07 ; Search time 35 Seconds
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19.036 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	10	21	AAB10010	H. pylori beta-ure
2	17	85.0	10	22	AAB86058	H. pylori beta-ure
3	17	85.0	10	22	AAB86090	H. pylori beta-ure
4	17	85.0	13	22	AAE05735	Complementarity-de
5	17	85.0	14	22	AAM98088	Human peptide #136
6	17	85.0	15	17	AAR97874	Japan cedar pollen
7	17	85.0	15	17	AAR97875	Japan cedar pollen
8	17	85.0	15	19	AAW57758	Residues 16-30 of
9	17	85.0	19	23	AAE23038	Human thioredoxin,
10	17	85.0	20	19	AAW42165	T-cell epitope pep
11	17	85.0	20	22	AAG62999	Complementarity de
12	17	85.0	27	22	AAM18617	Peptide #5051 enco
13	17	85.0	27	22	AAM31077	Peptide #5114 enco
14	17	85.0	27	23	ABG40522	Human peptide enco
15	17	85.0	29	21	AAB09301	Hepatitis GB virus
16	17	85.0	32	22	AAG71365	Human gene 10-enco
17	17	85.0	33	23	ABP60808	Sus scrofa thiored
18	17	85.0	34	15	AAR50631	G-protein coupled
19	17	85.0	34	15	AAR50593	G-protein coupled
20	17	85.0	34	17	AAW02785	G-protein coupled
21	17	85.0	34	17	AAW02823	G-protein coupled
22	17	85.0	35	22	AAO08042	Human polypeptide
23	17	85.0	36	15	AAR53693	Japanese cedar pol
24	17	85.0	37	22	AAO08979	Human polypeptide
25	17	85.0	38	21	AAG10451	Arabidopsis thalia
26	17	85.0	38	21	AAY76339	Fragment of human
27	17	85.0	40	20	AAY41113	TNFR/NGFR cysteine
28	17	85.0	40	21	AAG51555	Arabidopsis thalia
29	17	85.0	40	22	AAM64830	Human brain expres
30	17	85.0	40	22	AAO06835	Human polypeptide
31	17	85.0	40	22	AAM37764	Peptide #11801 enc
32	17	85.0	40	22	AAB64755	Human secreted pro
33	17	85.0	40	23	ABG46611	Human peptide enco
34	17	85.0	41	15	AAR53692	Japanese cedar pol
35	17	85.0	41	22	AAO07778	Human polypeptide
36	17	85.0	44	22	ABB29389	Peptide #2040 enco
37	17	85.0	44	22	ABB34562	Peptide #2068 enco
38	17	85.0	44	22	ABB19970	Protein #1969 enco
39	17	85.0	44	22	AAM55349	Human brain expres
40	17	85.0	44	22	AAM67745	Human bone marrow
41	17	85.0	44	22	AAO12937	Human polypeptide
42	17	85.0	44	22	AAM15556	Peptide #1990 enco
43	17	85.0	44	22	AAM28045	Peptide #2082 enco
44	17	85.0	45	15	AAR53691	Japanese cedar pol
45	17	85.0	46	22	ABB29210	Peptide #1861 enco

ALIGNMENTS

RESULT 1
AAB10010
ID AAB10010 standard; Protein; 10 AA.
XX
AC AAB10010;
XX
DT 01-NOV-2000 (first entry)
XX
DE H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2.
XX
KW Acid-resistant microorganism; detection; faecal; intestine; infection;
KW monoclonal antibody; heavy chain; complementarity determining region;
KW CDR; beta-urease.
XX
OS Unidentified.
XX
PN WO200026671-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-EP08212.
XX
PR 29-OCT-1998; 98EP-0120517.
PR 06-NOV-1998; 98EP-0120687.
XX
PA (CONN-) CONNEX GMBH.
XX
PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
PI Ringeis A;
XX
DR WPI; 2000-365747/31.
DR N-PSDB; AAA40166.
XX

PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
PT pylori, comprises reacting a faecal sample with two binding reagents for
PT antigens that survive intestinal passage -
XX
PS Claim 26; Page 22; 84pp; German.
XX
CC This invention describes a novel method for the detection of a mammalian
CC infection by an acid-resistant microorganism (A) by treating a faecal
CC sample with at least two different monoclonal antibodies (MAb) (or their
CC fragments or derivatives) or aptamers (collectively (I)) and detecting
CC formation of a complex (C) between (I) and the corresponding antigen of
CC (A). The first and second (I) bind to epitopes of different antigens
CC (Ag). These epitopes are present, after passage through the intestines,
CC in at least some mammals, and have either: (i) their native structure;
CC or (ii) a structure against which an antibody is produced by an animal
CC infected or immunized with (A), or its extract, lysate, derived protein
CC or fragment, or with a synthetic peptide. Practically all mammals display
CC at least one of the specified epitopes. The method is used to detect
CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,
CC M. tuberculosis, C. jejuni and C. pylori. (I) may also be used
CC therapeutically. The method is direct and non-invasive, and provides an
CC inexpensive and easily standardizable diagnosis, despite possible
CC degradation of antigens during passage through the intestines. This
CC sequence represents a fragment of a H. pylori beta-urease-binding
CC antibody heavy chain complementarity determining region CDR1 which is
CC used to illustrate the method of the invention.
XX
SQ Sequence 10 AA;

Query Match 85.0%; Score 17; DB 21; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FSTSW 8

RESULT 2
AAB86058
ID AAB86058 standard; Peptide; 10 AA.
XX
AC AAB86058;
XX
DT 17-JUL-2001 (first entry)
XX
DE H. pylori beta-urease derived antibody light chain CDR1 #1.
XX
KW Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;
KW antibacterial; complementarity determining region.
XX
OS Unidentified.
XX
PN WO200127613-A2.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-EP10058.
XX
PR 12-OCT-1999; 99EP-0120351.
PR 16-MAR-2000; 2000EP-0105592.
PR 31-MAR-2000; 2000EP-0107028.
PR 10-MAY-2000; 2000EP-0110110.
XX
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI Reiter C, Cullmann G, Heppner P, Ringeis A, Mueller H, Haindl E;
XX
DR WPI; 2001-282087/29.
DR N-PSDB; AAF88060.
XX

PT Detecting infections by acid-resistant microorganisms, particularly for
PT diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
PT sample -
XX
PS Claim 23; Page 17; 89pp; German.
XX
CC This invention describes a novel method for detecting, in a mammal,
CC infection by an acid-resistant microorganism (A) which comprises reacting
CC a fecal sample with: (i) a receptor (R) such that a complex is formed
CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part
CC complex is formed with Ag, and the formation of a complex detected. R are
CC specific for an Ag which, after passage through the intestines, at least
CC in some mammals, retains a native (or corresponding) structure against
CC which the mammal produces antibodies (when immunized or infected with
CC (A), or its extracts, lysates or derived proteins (or fragments) or
CC synthetic peptides). The products of the invention have antibacterial
CC activity. The method is used to diagnose infection by Helicobacter,
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the
CC progress of treatment. Receptors, particularly antibodies, directed
CC against Ag can be used therapeutically for treatment of infections. The
CC method requires only one R to provide a reasonably secure diagnosis
CC (although use of two R improves sensitivity), so is relatively
CC inexpensive and more easily standardized. Also it is direct,
CC non-invasive, suitable for automation and may indicate the stage of an
CC infection. This sequence represents a complementarity determining region
CC (CDR) from an antibody generated against a Helicobacter pylori antigen
CC (catalase or beta-urease) which is used to illustrate the method of the
CC invention.
XX
SQ Sequence 10 AA;

Query Match 85.0%; Score 17; DB 22; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FSTSW 8

RESULT 3
AAB86090
ID AAB86090 standard; Peptide; 10 AA.
XX
AC AAB86090;
XX
DT 17-JUL-2001 (first entry)
XX
DE H. pylori beta-urease derived antibody light chain CDR1 #1.
XX
KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
KW acid-resistant microorganism; complementarity determining region;
KW CDR; feces; heavy chain; light chain.
XX
OS Unidentified.
XX
PN WO200127612-A2.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-EP10057.
XX
PR 12-OCT-1999; 99EP-0120351.
PR 16-MAR-2000; 2000EP-0105592.
PR 31-MAR-2000; 2000EP-0107028.
PR 10-MAY-2000; 2000EP-0110110.
XX
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;
XX
DR WPI; 2001-282086/29.

```
DR   N-PSDB; AAF88117.
XX
PT   Detecting infections by acid-resistant microorganisms, particularly for
PT   diagnosing Helicobacter pylori, comprises immunochromatographic
PT   detection of antigen in feces -
XX
PS   Claim 27; Page 27; 90pp; German.
XX
CC   This invention describes a novel method for detecting infection by an
CC   acid-resistant microorganism (A), in a mammal, using
CC   immunochromatography. The method is used to diagnose infection by an
CC   acid-resistant microorganism (A), in a mammal, such as Helicobacter,
CC   Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC   H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
CC   inexpensive and non-invasive, and may indicate the stage of infection.
CC   A test strip used in the method may include a filter to eliminate
CC   particles present in the sample and only a single receptor provides a
CC   reasonably secure diagnosis, with specificity and selectivity improved
CC   by detecting several epitopes (of catalase) or different antigens
CC   (catalase and beta-urease). The method can be automated. This sequence
CC   represents a complementarity determining region (CDR) from an antibody
CC   raised against the H. pylori catalase or beta-urease antigen which is
CC   used to illustrate the method of the invention.
XX
SQ   Sequence   10 AA;

  Query Match             85.0%;  Score 17;  DB 22;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.5e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
            |   |
Db       4 FSTSW 8


RESULT 4
AAE05735
ID   AAE05735 standard; peptide; 13 AA.
XX
AC   AAE05735;
XX
DT   24-SEP-2001  (first entry)
XX
DE   Complementarity-determining region 3 (CDR3) of MoPhabs #7.
XX
KW   CDR3; complementarity-determining region 3; monoclonal phage antibody;
KW   MoPhabs; antigen.
XX
OS   Synthetic.
XX
PN   US6265150-B1.
XX
PD   24-JUL-2001.
XX
PF   26-MAY-1998;   98US-0085072.
XX
PR   07-JUN-1995;   95US-0483633.
PR   18-SEP-1997;   97US-0932892.
XX
PA   (BECT ) BECTON DICKINSON & CO.
PA   (CRUC-) CRUCELL HOLLAND BV.
XX
PI   Terstappen LW,  Logtenberg T;
XX
DR   WPI; 2001-463929/50.
XX
PT   Obtaining a phage particle, useful for obtaining human antibodies
PT   against known and novel surface antigens, by incubating a phage library
PT   with target cells to allow binding of the antibody fragment to the
PT   antigen -
XX
PS   Example 6; Column 6; 6pp; English.
XX
CC   The invention relates to a method of obtaining a phage particle
CC   which has an antibody fragment directed against an antigen associated
CC   with the surface of target cells in a heterogeneous cell population.
CC   The method involves incubating a library of phage particles with the
CC   target cells to allow binding of the antibody fragment expressed on
CC   the surface of the phage particles to the antigen associated with
CC   the target cells. The method is useful for obtaining human antibodies
CC   against known and novel surface antigens in their native configuration,
CC   expressed on phenotypically defined subpopulations of cells.
CC   The present sequence is complementarity-determining region 3 (CDR3)
CC   of monoclonal phage antibodies (MoPhabs) used in the exemplification
CC   of the invention.
XX
SQ   Sequence   13 AA;

  Query Match             85.0%;  Score 17;  DB 22;  Length 13;
  Best Local Similarity   40.0%;  Pred. No. 1.8e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
            |   |
Db       6 FASSW 10


RESULT 5
AAM98088
ID   AAM98088 standard; Peptide; 14 AA.
XX
AC   AAM98088;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human peptide #1363 encoded by a SNP oligonucleotide.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;   99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections -
XX
PS   Disclosure; Page 3967; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC   encoding polymorphic variants of proteins related to amylases, amyloid
CC   proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
CC   polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC   complement related proteins, cytochromes, kinesins, cytokines,
CC   interferons, interleukins, G-protein coupled receptors and thioesterases.
CC   The present sequence is a peptide encoded by one such oligonucleotide.
```

```
CC   The oligonucleotides and the peptides encoded by them may be used in the
CC   prevention, diagnosis and treatment of diseases associated with
CC   inappropriate expression of the proteins listed above. Disorders that may
CC   be prevented, diagnosed and/or treated include multifactorial diseases
CC   with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC   arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
CC   and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC   brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC   system and an infection of pathogenic organisms.
XX
SQ   Sequence   14 AA;

  Query Match             85.0%;  Score 17;  DB 22;  Length 14;
  Best Local Similarity   40.0%;  Pred. No. 2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       6 FASTW 10


RESULT 6
AAR97874
ID   AAR97874 standard; peptide; 15 AA.
XX
AC   AAR97874;
XX
DT   16-AUG-1996  (first entry)
XX
DE   Japan cedar pollen mature allergen Cry j II amino acids 16-30.
XX
KW   Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
KW   Sugi pollinosis; diagnosis; treatment.
XX
OS   Cryptomeria japonica.
XX
PN   JP08047392-A.
XX
PD   20-FEB-1996.
XX
PF   07-NOV-1994;   94JP-0297840.
XX
PR   26-MAY-1994;   94JP-0134868.
PR   05-NOV-1993;   93JP-0276773.
XX
PA   (MEIP ) MEIJI MILK PROD CO LTD.
XX
DR   WPI; 1996-166249/17.
XX
PT   Japan cedar pollen allergen Cry j II epitope - comprises at least
PT   part of specified 460 amino acid protein
XX
PS   Claim 8; Fig 3; 17pp; Japanese.
XX
CC   AAR97871-R97960 are overlapping peptides used for the epitope mapping
CC   of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
CC   peptides of it are useful in the diagnosis, prevention and treatment
CC   of Sugi pollinosis, the allergic reaction to Japan cedar pollen.
CC   Significant regions of the allergen were identified using the
CC   overlapping peptides of the full epitope derived from a Cry j II
CC   antigen-specific T cell line. Amino acids 66-80 (AAR97884) and 186-200
CC   (R978908) of the full mature 460 amino acid allergen are the most
CC   allergenic of the 90 peptides tested.
XX
SQ   Sequence   15 AA;

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       9 FSTAW 13


RESULT 7
AAR97875
ID   AAR97875 standard; peptide; 15 AA.
XX
AC   AAR97875;
XX
DT   16-AUG-1996  (first entry)
XX
DE   Japan cedar pollen mature allergen Cry j II amino acids 21-35.
XX
KW   Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
KW   Sugi pollinosis; diagnosis; treatment.
XX
OS   Cryptomeria japonica.
XX
PN   JP08047392-A.
XX
PD   20-FEB-1996.
XX
PF   07-NOV-1994;   94JP-0297840.
XX
PR   26-MAY-1994;   94JP-0134868.
PR   05-NOV-1993;   93JP-0276773.
XX
PA   (MEIP ) MEIJI MILK PROD CO LTD.
XX
DR   WPI; 1996-166249/17.
XX
PT   Japan cedar pollen allergen Cry j II epitope - comprises at least
PT   part of specified 460 amino acid protein
XX
PS   Claim 8; Fig 3; 17pp; Japanese.
XX
CC   AAR97871-R97960 are overlapping peptides used for the epitope mapping
CC   of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
CC   peptides of it are useful in the diagnosis, prevention and treatment
CC   of Sugi pollinosis, the allergic reaction to Japan cedar pollen.
CC   Significant regions of the allergen were identified using the
CC   overlapping peptides of the full epitope derived from a Cry j II
CC   antigen-specific T cell line. Amino acids 66-80 (AAR97884) and 186-200
CC   (R978908) of the full mature 460 amino acid allergen are the most
CC   allergenic of the 90 peptides tested.
XX
SQ   Sequence   15 AA;

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSTAW 8


RESULT 8
AAW57758
ID   AAW57758 standard; peptide; 15 AA.
XX
AC   AAW57758;
XX
DT   17-SEP-1998  (first entry)
XX
DE   Residues 16-30 of Cry j 2.
XX
KW   Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;
KW   HLA class II molecule.
XX
OS   Cryptomeria japonica.
XX
PN   WO9820902-A1.
XX
```

PD 22-MAY-1998.
XX
PF 12-NOV-1997; 97WO-JP04129.
XX
PR 13-NOV-1996; 96JP-0302053.
XX
PA (MEIP) MEIJI MILK PROD CO LTD.
XX
PI Dairiki K, Kino K, Kume A, Sone T;
XX
DR WPI; 1998-297617/26.
XX
PT Peptides derived from Japanese cedar pollen antigens are
PT immunotherapeutic agents - useful for allergy treatment and typing
PT HLA class II molecules in allergy sufferers
XX
PS Claim 12; Page 29; 50pp; Japanese.
XX
CC This sequence represents residues 16-30 of the Cry j 2 protein, and
CC is a peptide of the invention. The peptides are derived from Japanese
CC cedar pollen antigens, and are used as immunotherapeutic agents in the
CC treatment of allergy. The peptides can be used for identification and
CC typing of the particular HLA class II molecules in an allergy sufferer,
CC and also for peptide immunotherapy of an allergy. Using these peptides
CC the immunotherapy can be targeted more specifically to the requirements
CC of the individual patient, allowing more effective treatment of an
CC allergy, including those patients for whom treatment with a conventional
CC immunotherapeutic agent is ineffective.
XX
SQ Sequence 15 AA;

Query Match 85.0%; Score 17; DB 19; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 9 FSTAW 13

RESULT 9
AAE23038
ID AAE23038 standard; peptide; 19 AA.
XX
AC AAE23038;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human thioredoxin, 47916 peptide.
XX
KW Human; thioredoxin; 22108; 47916; haematopoietic disorder; leukaemia;
KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;
KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;
KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;
KW cytostatic; carcinoma; cardiant; neuroprotective; antiinflammatory;
KW gene therapy; nootropic.
XX
OS Homo sapiens.
XX
PN WO200226803-A2.
XX
PD 04-APR-2002.
XX
PF 25-SEP-2001; 2001WO-US29967.
XX
PR 25-SEP-2000; 2000US-235049P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Bandaru R, Kapeller-Libermann R;
XX
DR WPI; 2002-416475/44.
XX
PT New human thioredoxin nucleic acid and polypeptide molecules,
PT designated 22108 and 47916, useful for diagnosing, preventing or
PT treating cancer (e.g. carcinoma), cardiovascular diseases (e.g. heart
PT failure) or brain disorders -
XX
PS Disclosure; Page 11; 124pp; English.
XX
CC The invention relates to human thioredoxin nucleic acid and polypeptide
CC molecules, designated 22108 and 47916. The compound that modulates the
CC activity or expression of 22108 and 47916 nucleic acid is useful for
CC treating or preventing a disorder characterised by aberrant activity of
CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting
CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The
CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,
CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,
CC metastatic or haematopoietic disorders (e.g.leukaemia), or cancers of
CC the lung, breast, thyroid, head neck, prostate or genito-urinary tract),
CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart
CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's
CC diseases). The thioredoxin DNA is also useful in gene therapy. The
CC present sequence is human thioredoxin, 47916 peptide.
XX
SQ Sequence 19 AA;

Query Match 85.0%; Score 17; DB 23; Length 19;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FSATW 8

RESULT 10
AAW42165
ID AAW42165 standard; peptide; 20 AA.
XX
AC AAW42165;
XX
DT 16-JUN-1998 (first entry)
XX
DE T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.
XX
KW Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;
KW diagnosis; allergy; spring tree pollen disease; pollinosis.
XX
OS Chamaeyparis obtusa.
XX
PN WO9747648-A1.
XX
PD 18-DEC-1997.
XX
PF 12-JUN-1997; 97WO-JP02031.
XX
PR 14-JUN-1996; 96JP-0153527.
XX
PA (MEIP) MEIJI MILK PROD CO LTD.
XX
PI Dairiki K, Kino K;
XX
DR WPI; 1998-052242/05.
XX
PT T-cell epitope peptide portion of Japanese cypress pollen antigens
PT Chao1 and Chao2 - used for diagnosis and treatment of spring tree
PT pollen disease
XX
PS Claim 2; Page 36; 71pp; Japanese.
XX
CC The present sequence represents a T-cell epitope peptide from Japanese
CC cypress pollen antigen Chao2. The present invention describes peptides
CC which correspond to the T-cell epitope sites on Japanese cypress pollen
CC antigens Chao1 and Chao2. The peptides can be used as a reagent for the
CC diagnosis of allergy to Japanese cypress pollen, and as an antigen in

```
CC   the treatment and prevention of spring tree pollen disease in which the
CC   pollinosis involves reactivity to Japanese cypress pollen.
XX
SQ   Sequence   20 AA;

  Query Match             85.0%;  Score 17;  DB 19;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 2.6e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       8 FATTW 12


RESULT 11
AAG62999
ID   AAG62999 standard; peptide; 20 AA.
XX
AC   AAG62999;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Complementarity determining region 3 (CDR3) of VH chain of clone G101.
XX
KW   Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW   endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW   transferrin receptor; neurological disease; Alzheimer's disease;
KW   prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS   Homo sapiens.
XX
PN   WO200144300-A2.
XX
PD   21-JUN-2001.
XX
PF   27-NOV-2000; 2000WO-GB04501.
XX
PR   13-DEC-1999;   99US-0170599.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Webster C,  Osbourn J,  Ward G,  Miller K;
XX
DR   WPI; 2001-398131/42.
XX
PT   Mixture or panel of antibodies for selecting specific binding members
PT   that cross the blood brain barrier, for use in delivering different
PT   molecules and treating neurological diseases  -
XX
PS   Claim 1; Page 76; 109pp; English.
XX
CC   AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC   of VL and VH chains of antibodies of the invention. The specification
CC   describes a mixture or panel of 5 different specific binding members,
CC   each comprising an antibody VH and/or VL variable domain and capable,
CC   when displayed on the surface of filamentous bacteriophage particles or
CC   in the case of a specific binding member comprising the D5 VH and/or VL
CC   variable domain when bound to human serum amyloid protein, to pass
CC   through a mammalian blood brain barrier (BBB). The panel is useful for
CC   the selection of specific binding members with a desired property such
CC   as ability to cross BBB, ability to bind endothelial cells or other brain
CC   cell antigen, ability to bind areas of inflammation in the brain or BBB
CC   breakdown or ability to bind intracellular adhesion molecules and to bind
CC   transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC   and treatment of human or animal body, including neurological diseases,
CC   such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC   epilepsy and traumatic brain injury and any diseases involving
CC   inflammation occurring within the brain or central nervous system.
XX
SQ   Sequence   20 AA;

  Query Match             85.0%;  Score 17;  DB 22;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 2.6e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSSSW 8


RESULT 12
AAM18617
ID   AAM18617 standard; Protein; 27 AA.
XX
AC   AAM18617;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Peptide #5051 encoded by probe for measuring cervical gene expression.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00670.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human cervical epithelial cells -
XX
PS   Claim 27; SEQ ID No 23443; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC   by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC   can be used to produce a single exon microarray, which can be used for
CC   measuring human gene expression in a sample derived from human cervical
CC   epithelial cells. By measuring gene expression, the probes are therefore
CC   useful in grading and/or staging of diseases of the cervix, notably
CC   cervical cancer.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   27 AA;

  Query Match             85.0%;  Score 17;  DB 22;  Length 27;
  Best Local Similarity   40.0%;  Pred. No. 3.3e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSATW 8


RESULT 13
AAM31077
ID   AAM31077 standard; Protein; 27 AA.
```

XX
AC AAM31077;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #5114 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 27; SEQ ID No 31346; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
SQ Sequence 27 AA;

Query Match 85.0%; Score 17; DB 22; Length 27;
Best Local Similarity 40.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FSATW 8

RESULT 14
ABG40522
ID ABG40522 standard; Peptide; 27 AA.
XX
AC ABG40522;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 30187.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesis; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US00665.
XX
PR 04-FEB-2000; 2000US-180312P.
PR 26-MAY-2000; 2000US-207456P.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
PS Claim 27; SEQ ID No 30187; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis,
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a peptide/protein
CC encoded by a single exon probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 27 AA;

Query Match 85.0%; Score 17; DB 23; Length 27;

Best Local Similarity 40.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1 FXXXW 5
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Db       4 FSATW 8
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RESULT 15
AAB09301
ID AAB09301 standard; Protein; 29 AA.
XX
AC AAB09301;
XX
DT 30-AUG-2000 (first entry)
XX
DE Hepatitis GB virus protein sequence SEQ ID NO:428.
XX
KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic;
KW infection; detection; characterisation; hepatitis.
XX
OS Hepatitis GB virus.
XX
PN US6051374-A.
XX
PD 18-APR-2000.
XX
PF 07-JUN-1995; 95US-0488445.
XX
PR 14-FEB-1994; 94US-0196030.
PR 13-MAY-1994; 94US-0242654.
PR 29-JUL-1994; 94US-0283314.
PR 23-NOV-1994; 94US-0344185.
PR 23-NOV-1994; 94US-0344190.
PR 30-JAN-1995; 95US-0377557.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
XX
DR WPI; 2000-338307/29.
XX
PT Detecting target hepatitis GB virus nucleic acid in a test sample
PT suspected of containing HGBV comprises reacting the test sample the
PT HGBV polynucleotide probe and detecting the complex that contains
PT target HGBV -
XX
PS Example 18; Column 491-492; 369pp; English.
XX
CC The present invention describe a method for detecting target
CC hepatitis GB virus (HGBV) nucleic acid (THN) in a test sample (T)
CC suspected of containing HGBV. The method involves reacting (T) with a
CC HGBV polynucleotide probe (I) containing 15 contiguous nucleotides, and
CC which selectively hybridises to the HGBV genome or its full complement,
CC and detecting the complex that contains THN, indicating the presence of
CC target HGBV. The method is used for detecting target HGBV nucleic acid
CC in the test sample suspected of containing HGBV and for characterisation
CC of newly ascertained etiological agent of non-A, non-B, non-C, non-D and
CC non-E hepatitis causing agents collectively termed as hepatitis GB
CC virus. AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide
CC and protein sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 29 AA;

Query Match 85.0%; Score 17; DB 21; Length 29;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1 FXXXW 5
           |   |
Db      12 FASAW 16
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Search completed: January 29, 2003, 14:11:20
Job time : 36 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2003, 14:12:18 ; Search time 11 Seconds
(without alignments)
9.172 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	27	10	US-09-864-761-46828	Sequence 46828, A
2	17	85.0	29	8	US-08-424-550B-428	Sequence 428, App
3	17	85.0	40	10	US-09-057-951-6	Sequence 6, Appli
4	17	85.0	40	10	US-09-864-761-46093	Sequence 46093, A
5	17	85.0	40	12	US-10-105-150-6	Sequence 6, Appli
6	17	85.0	44	10	US-09-864-761-35268	Sequence 35268, A
7	17	85.0	46	10	US-09-864-761-35084	Sequence 35084, A
8	17	85.0	71	10	US-09-864-761-45867	Sequence 45867, A
9	17	85.0	75	10	US-09-867-550-510	Sequence 510, App
10	17	85.0	77	12	US-10-001-843-186	Sequence 186, App
11	17	85.0	78	10	US-09-864-761-33877	Sequence 33877, A
12	17	85.0	104	9	US-10-032-482-1	Sequence 1, Appli
13	17	85.0	111	10	US-09-925-300-980	Sequence 980, App
14	17	85.0	114	10	US-09-897-898-6	Sequence 6, Appli
15	17	85.0	114	10	US-09-992-524-9	Sequence 9, Appli
16	17	85.0	114	10	US-09-992-524-10	Sequence 10, Appl
17	17	85.0	114	10	US-09-992-524-11	Sequence 11, Appl
18	17	85.0	125	10	US-09-925-300-1114	Sequence 1114, Ap
19	17	85.0	134	9	US-10-079-623-364	Sequence 364, App
20	17	85.0	135	10	US-09-925-299-878	Sequence 878, App
21	17	85.0	136	10	US-09-992-524-4	Sequence 4, Appli
22	17	85.0	136	10	US-09-992-524-8	Sequence 8, Appli
23	17	85.0	169	10	US-09-897-898-9	Sequence 9, Appli
24	17	85.0	174	10	US-09-764-877-1745	Sequence 1745, Ap
25	17	85.0	181	8	US-08-870-434-10	Sequence 10, Appl
26	17	85.0	182	8	US-08-825-486-8	Sequence 8, Appli
27	17	85.0	182	10	US-09-372-044-8	Sequence 8, Appli
28	17	85.0	192	10	US-09-864-761-33690	Sequence 33690, A
29	17	85.0	232	10	US-09-897-898-11	Sequence 11, Appl
30	17	85.0	241	10	US-09-815-242-10985	Sequence 10985, A
31	17	85.0	247	9	US-09-908-193-42	Sequence 42, Appl
32	17	85.0	248	9	US-09-908-193-41	Sequence 41, Appl
33	17	85.0	249	9	US-09-908-193-16	Sequence 16, Appl
34	17	85.0	258	9	US-09-813-453A-6	Sequence 6, Appli
35	17	85.0	268	10	US-09-764-864-1258	Sequence 1258, Ap
36	17	85.0	270	10	US-09-764-864-1433	Sequence 1433, Ap
37	17	85.0	271	9	US-09-479-040-23	Sequence 23, Appl
38	17	85.0	273	10	US-09-893-737-294	Sequence 294, App
39	17	85.0	289	10	US-09-815-242-5556	Sequence 5556, Ap
40	17	85.0	293	10	US-09-925-301-1119	Sequence 1119, Ap
41	17	85.0	297	9	US-09-738-626-6265	Sequence 6265, Ap
42	17	85.0	313	10	US-09-886-055-415	Sequence 415, App
43	17	85.0	324	10	US-09-966-264-31	Sequence 31, Appl
44	17	85.0	328	10	US-09-815-242-12495	Sequence 12495, A
45	17	85.0	345	9	US-10-007-706-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-864-761-46828
; Sequence 46828, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

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;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46828
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC007739.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61
US-09-864-761-46828

  Query Match             85.0%;  Score 17;  DB 10;  Length 27;
  Best Local Similarity   40.0%;  Pred. No. 5.7e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
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Db       4 FSATW 8


RESULT 2
US-08-424-550B-428
; Sequence 428, Application US/08424550B
; Patent No. US20020119447A1
;  GENERAL INFORMATION:
;    APPLICANT:  JOHN N. SIMONS
;    APPLICANT:  TAMI J. PILOT-MATIAS
;    APPLICANT:  GEORGE J. DAWSON
;    APPLICANT:  GEORGE G. SCHLAUDER
;    APPLICANT:  SURESH M. DESAI
;    APPLICANT:  THOMAS P. LEARY
;    APPLICANT:  ANTHONY SCOTT MUERHOFF
;    APPLICANT:  JAMES C. ERKER
;    APPLICANT:  SHERI L. BUIJK
;    APPLICANT:  ISA K. MUSHAHWAR
;    TITLE OF INVENTION:  NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
;    TITLE OF INVENTION:  REAGENTS AND METHODS FOR THEIR USE
;    NUMBER OF SEQUENCES:  716
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ABBOTT LABORATORIES  D377/AP6D
;      STREET:  100 ABBOTT PARK ROAD
;      CITY:  ABBOTT PARK
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/424,550B
;      FILING DATE:
;      CLASSIFICATION:  435435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  POREMBSKI, PRISCILLA E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5527.PC.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-6365
;      TELEFAX:  708-938-2623
;  INFORMATION FOR SEQ ID NO:  428:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-424-550B-428

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  Best Local Similarity   40.0%;  Pred. No. 6e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      12 FASAW 16


RESULT 3
US-09-057-951-6
; Sequence 6, Application US/09057951
; Patent No. US20020025551A1
;  GENERAL INFORMATION:
;    APPLICANT:  Holtzman, Douglas
;    TITLE OF INVENTION:  NOVEL MOLECULES OF THE T129-RELATED
;    TITLE OF INVENTION:  PROTEIN FAMILY AND USES THEREOF
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,951
;      FILING DATE:  09-APR-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meiklejohn, Ph.D., Anita L.
;      REGISTRATION NUMBER:  35,283
;      REFERENCE/DOCKET NUMBER:  09404/046001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-057-951-6

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  Best Local Similarity   40.0%;  Pred. No. 7.4e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       6 FSAAW 10


RESULT 4
US-09-864-761-46093
; Sequence 46093, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
```

```
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
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;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46093
;    LENGTH: 40
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: MAP TO AF233390.1
;    OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;    OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
;    OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
;    OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
US-09-864-761-46093

  Query Match             85.0%;  Score 17;  DB 10;  Length 40;
  Best Local Similarity   40.0%;  Pred. No. 7.4e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      23 FTSSW 27


RESULT 5
US-10-105-150-6
; Sequence 6, Application US/10105150
; Patent No. US20020119524A1
;   GENERAL INFORMATION:
;        APPLICANT: Holtzman, Douglas
;        TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED
;                            PROTEIN FAMILY AND USES THEREOF
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 225 Franklin Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02110-2804
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/105,150
;             FILING DATE: 25-Mar-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/057,951
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Meiklejohn, Ph.D., Anita L.
;             REGISTRATION NUMBER: 35,283
;             REFERENCE/DOCKET NUMBER: 09404/046001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617/542-5070
;             TELEFAX: 617/542-8906
;             TELEX: 200154
;    INFORMATION FOR SEQ ID NO: 6:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 40 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-105-150-6

  Query Match             85.0%;  Score 17;  DB 12;  Length 40;
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  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
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Db       6 FSAAW 10


RESULT 6
US-09-864-761-35268
; Sequence 35268, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
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;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35268
;   LENGTH: 44
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC004852.2
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL =   1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
;   OTHER INFORMATION: EST_HUMAN HIT: AA320774.1, EVALUE 5.00e-10
;   OTHER INFORMATION: SWISSPROT HIT: P11369, EVALUE 1.00e-03
US-09-864-761-35268

  Query Match             85.0%;  Score 17;  DB 10;  Length 44;
  Best Local Similarity   40.0%;  Pred. No. 7.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |  |
Db      18 FAATW 22


RESULT 7
US-09-864-761-35084
; Sequence 35084, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35084
;   LENGTH: 46
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC007938.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.6
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.99
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
;   OTHER INFORMATION: EST_HUMAN HIT: BF642802.1, EVALUE 2.00e-19
;   OTHER INFORMATION: SWISSPROT HIT: P53620, EVALUE 5.00e-15
US-09-864-761-35084

  Query Match             85.0%;  Score 17;  DB 10;  Length 46;
  Best Local Similarity   40.0%;  Pred. No. 8.1e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |  |
Db      20 FAAAW 24


RESULT 8
US-09-864-761-45867
; Sequence 45867, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
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;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45867
;   LENGTH: 71
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL121827.9
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.51
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.51
;   OTHER INFORMATION: SWISSPROT HIT: Q63262, EVALUE 4.40e-01
;   OTHER INFORMATION: EST_HUMAN HIT: AW151498.1, EVALUE 1.00e+00
US-09-864-761-45867

  Query Match             85.0%;  Score 17;  DB 10;  Length 71;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FASSW 8


RESULT 9
US-09-867-550-510
; Sequence 510, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin D.
;  APPLICANT:  Mehraban, Fuad,
;  APPLICANT:  Conley, Pamela
;  APPLICANT:  Law, Debbie
;  APPLICANT:  Topper, James
;  TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
;  TITLE OF INVENTION:  Thereby
;  FILE REFERENCE: 21402-013 (Cura-313)
;  CURRENT APPLICATION NUMBER: US/09/867,550
;  CURRENT FILING DATE:  2001-09-20
;  PRIOR APPLICATION NUMBER: USSN 60/208,427
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 2125
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 510
;   LENGTH: 75
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-867-550-510

  Query Match             85.0%;  Score 17;  DB 10;  Length 75;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      64 FSSSW 68


RESULT 10
US-10-001-843-186
; Sequence 186, Application US/10001843
; Patent No. US20020132255A1
; GENERAL INFORMATION:
;  APPLICANT: Salceda, Susana
;  APPLICANT:  Macina, Roberto
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Cafferkey, Robert
;  APPLICANT:  Sun, Yongming
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Turner, Leah
;  TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
;  FILE REFERENCE: DEX-0267
;  CURRENT APPLICATION NUMBER: US/10/001,843
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: 60/249,992
;  PRIOR FILING DATE: 2000-11-20
;  NUMBER OF SEQ ID NOS: 218
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 186
;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-001-843-186

  Query Match             85.0%;  Score 17;  DB 12;  Length 77;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      63 FSASW 67


RESULT 11
US-09-864-761-33877
; Sequence 33877, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
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;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33877
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC007600.2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.7
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.76
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.68
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.81
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.96
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.97
;   OTHER INFORMATION: EST_HUMAN HIT: BE089591.1, EVALUE 4.00e-09
;   OTHER INFORMATION: SWISSPROT HIT: O15440, EVALUE 2.00e-08
US-09-864-761-33877

  Query Match             85.0%;  Score 17;  DB 10;  Length 78;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      39 FSSSW 43


RESULT 12
US-10-032-482-1
; Sequence 1, Application US/10032482
; Publication No. US20020197270A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Irun
;  APPLICANT:  ROTTER, Varda
;  APPLICANT:  Wolkowicz, Roland
;  APPLICANT:  RUIZ, Pedro
;  APPLICANT:  EREZ-ALON, Neta
;  APPLICANT:  HERKEL, Johannes
;  TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
;  TITLE OF INVENTION:  IMMUNITY
;  FILE REFERENCE: COHEN42
;  CURRENT APPLICATION NUMBER: US/10/032,482
;  CURRENT FILING DATE:  2002-01-02
;  PRIOR APPLICATION NUMBER: US/09/445,602
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: PCT/IL98/00266
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: IL 121041
;  PRIOR FILING DATE: 1997-06-09
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-032-482-1

  Query Match             85.0%;  Score 17;  DB 9;  Length 104;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      20 FTSSW 24


RESULT 13
US-09-925-300-980
; Sequence 980, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
;  APPLICANT: Craig Rosen,
;  APPLICANT:  Steve Ruben
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA101
;  CURRENT APPLICATION NUMBER: US/09/925,300
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05988
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1890
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 980
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (35)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-980

  Query Match             85.0%;  Score 17;  DB 10;  Length 111;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      52 FAASW 56


RESULT 14
US-09-897-898-6
; Sequence 6, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
;  APPLICANT: DECKERS, HARM M.
;  APPLICANT:  VAN ROOIJEN, GIJS
;  APPLICANT:  BOOTHE, JOSEPH
;  APPLICANT:  GOLL, JANIS
;  APPLICANT:  MOLONEY, MAURICE M.
```

```
;  APPLICANT:  DALMIA, BIPIN K.
;  TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
;  TITLE OF INVENTION:  BODY BASED PRODUCTS
;  FILE REFERENCE: 034547/0104
;  CURRENT APPLICATION NUMBER: US/09/897,898
;  CURRENT FILING DATE:  2001-09-21
;  PRIOR APPLICATION NUMBER: 09/577,147
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 09/448,600
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: 09/084,777
;  PRIOR FILING DATE: 1998-05-27
;  PRIOR APPLICATION NUMBER: 60/047,753
;  PRIOR FILING DATE: 1997-05-27
;  PRIOR APPLICATION NUMBER: 60/047,779
;  PRIOR FILING DATE: 1997-05-28
;  PRIOR APPLICATION NUMBER: 60/075,863
;  PRIOR FILING DATE: 1998-02-25
;  PRIOR APPLICATION NUMBER: 60/075,864
;  PRIOR FILING DATE: 1998-02-25
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 114
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-09-897-898-6

  Query Match             85.0%;  Score 17;  DB 10;  Length 114;
  Best Local Similarity   40.0%;  Pred. No. 1.5e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      35 FTASW 39


RESULT 15
US-09-992-524-9
; Sequence 9, Application US/09992524
; Patent No. US20020091240A1
; GENERAL INFORMATION:
;  APPLICANT: Vasquez, Maximiliano
;  APPLICANT:  Landolfi, Nicholas F.
;  APPLICANT:  Tsurushita, Naoya
;  APPLICANT:  Queen, Cary L.
;  APPLICANT:  Protein Design Labs, Inc.
;  TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
;  FILE REFERENCE: 011823-008110US
;  CURRENT APPLICATION NUMBER: US/09/992,524
;  CURRENT FILING DATE:  2001-11-13
;  PRIOR APPLICATION NUMBER: 09/450,520
;  PRIOR FILING DATE: 1999-11-29
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 114
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:humanized
;   OTHER INFORMATION: immunoglobulin huXAF
US-09-992-524-9

  Query Match             85.0%;  Score 17;  DB 10;  Length 114;
  Best Local Similarity   40.0%;  Pred. No. 1.5e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      29 FTSSW 33
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Job time : 12 secs

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OM protein - protein search, using sw model

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(without alignments)
23.360 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

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Maximum Match 100%
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24: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	9	24	US-10-072-419-3	Sequence 3, Appli
2	17	85.0	9	24	US-10-072-419-8	Sequence 8, Appli
3	17	85.0	10	22	US-09-842-776A-28	Sequence 28, Appl
4	17	85.0	10	24	US-10-089-452-36	Sequence 36, Appl
5	17	85.0	10	25	US-10-110-410-36	Sequence 36, Appl
6	17	85.0	11	24	US-10-072-419-37	Sequence 37, Appl
7	17	85.0	14	17	US-09-355-397C-36	Sequence 36, Appl
8	17	85.0	15	17	US-09-308-027-12	Sequence 12, Appl
9	17	85.0	15	17	US-09-308-027-88	Sequence 88, Appl
10	17	85.0	15	17	US-09-308-027A-12	Sequence 12, Appl
11	17	85.0	15	17	US-09-308-027A-88	Sequence 88, Appl
12	17	85.0	19	23	US-09-963-339-10	Sequence 10, Appl
13	17	85.0	19	25	US-10-145-586-59	Sequence 59, Appl
14	17	85.0	20	16	US-09-202-464-45	Sequence 45, Appl
15	17	85.0	20	16	US-09-240-203B-265	Sequence 265, App
16	17	85.0	20	16	US-09-240-203D-265	Sequence 265, App
17	17	85.0	21	4	US-08-074-180B-95	Sequence 95, Appl
18	17	85.0	22	7	US-08-344-185B-275	Sequence 275, App
19	17	85.0	22	7	US-08-344-185C-275	Sequence 275, App
20	17	85.0	24	16	US-09-240-203B-264	Sequence 264, App
21	17	85.0	24	16	US-09-240-203D-264	Sequence 264, App
22	17	85.0	27	1	PCT-US01-00663-31346	Sequence 31346, A
23	17	85.0	27	22	US-09-864-761-46828	Sequence 46828, A
24	17	85.0	27	25	US-10-182-997-23443	Sequence 23443, A
25	17	85.0	27	26	US-10-203-135-30187	Sequence 30187, A
26	17	85.0	27	26	US-10-203-136-31135	Sequence 31135, A
27	17	85.0	27	26	US-10-203-137-31346	Sequence 31346, A
28	17	85.0	27	27	US-60-236-359-21109	Sequence 21109, A
29	17	85.0	28	27	US-60-162-245-3999	Sequence 3999, Ap
30	17	85.0	29	8	US-08-424-550A-428	Sequence 428, App
31	17	85.0	29	8	US-08-424-550B-428	Sequence 428, App
32	17	85.0	29	8	US-08-467-344A-428	Sequence 428, App
33	17	85.0	29	8	US-08-486-749-428	Sequence 428, App
34	17	85.0	29	8	US-08-488-445A-428	Sequence 428, App
35	17	85.0	29	8	US-08-488-446-428	Sequence 428, App
36	17	85.0	30	21	US-09-758-462-1651	Sequence 1651, Ap
37	17	85.0	30	26	US-10-212-059-1651	Sequence 1651, Ap
38	17	85.0	32	1	PCT-US00-29360-216	Sequence 216, App
39	17	85.0	33	24	US-10-029-386-28347	Sequence 28347, A
40	17	85.0	33	24	US-10-032-201B-157	Sequence 157, App
41	17	85.0	34	20	US-09-614-450-3288	Sequence 3288, Ap
42	17	85.0	35	20	US-09-617-682A-10658	Sequence 10658, A
43	17	85.0	36	1	PCT-US93-11000-5	Sequence 5, Appli
44	17	85.0	36	3	US-07-975-179A-5	Sequence 5, Appli
45	17	85.0	36	6	US-08-226-248A-137	Sequence 137, App

ALIGNMENTS

RESULT 1
US-10-072-419-3
; Sequence 3, Application US/10072419
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in H
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-072-419-3

Query Match 85.0%; Score 17; DB 24; Length 9;
Best Local Similarity 40.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FTSSW 8

RESULT 2
US-10-072-419-8

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; Sequence 8, Application US/10072419
; GENERAL INFORMATION:
;  APPLICANT: Schacter, Bernice
;  APPLICANT:  Schacter, Lee
;  TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Huma
;  FILE REFERENCE: 10739-1
;  CURRENT APPLICATION NUMBER: US/10/072,419
;  CURRENT FILING DATE:  2002-02-07
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Vanessa cardui
US-10-072-419-8

  Query Match             85.0%;  Score 17;  DB 24;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 4.2e+06;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      4 FTSSW 8


RESULT 3
US-09-842-776A-28
; Sequence 28, Application US/09842776A
; GENERAL INFORMATION:
;  APPLICANT: CONNEX GMBH
;  TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
;  TITLE OF INVENTION:  IN THE STOOL
;  FILE REFERENCE: 41735
;  CURRENT APPLICATION NUMBER: US/09/842,776A
;  CURRENT FILING DATE:  2002-08-15
;  PRIOR APPLICATION NUMBER: PCT/EP99/08212
;  PRIOR FILING DATE: 1999-10-29
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Complementarity determining region (CDR1) of an
;   OTHER INFORMATION: antibody heavy chain directed to a beta-urease
;   OTHER INFORMATION: epitope (alternative sequence)
US-09-842-776A-28

  Query Match             85.0%;  Score 17;  DB 22;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.6e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      4 FSTSW 8


RESULT 4
US-10-089-452-36
; Sequence 36, Application US/10089452
; GENERAL INFORMATION:
;  APPLICANT: Connex Gesellschaft zur Optimierung von Forschung und Entwicklung mbH
;  TITLE OF INVENTION: Improved Method for Detecting Acid Resistant Microorganisms in th
;  FILE REFERENCE: D 2394 PCT
;  CURRENT APPLICATION NUMBER: US/10/089,452
;  CURRENT FILING DATE:  2002-03-29
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: CDR
US-10-089-452-36

  Query Match             85.0%;  Score 17;  DB 24;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.6e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      4 FSTSW 8


RESULT 5
US-10-110-410-36
; Sequence 36, Application US/10110410
; GENERAL INFORMATION:
;  APPLICANT: Connex Gesellschaft zur Optimierung von Forschung und Entwicklung mbH
;  TITLE OF INVENTION: Immunochromatographic Rapid Test for Detecting Acid Resistant
;  TITLE OF INVENTION:  Microorganisms in the Stool
;  FILE REFERENCE: D 1805 PCT
;  CURRENT APPLICATION NUMBER: US/10/110,410
;  CURRENT FILING DATE:  2002-04-12
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: CDR
US-10-110-410-36

  Query Match             85.0%;  Score 17;  DB 25;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.6e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      4 FSTSW 8


RESULT 6
US-10-072-419-37
; Sequence 37, Application US/10072419
; GENERAL INFORMATION:
;  APPLICANT: Schacter, Bernice
;  APPLICANT:  Schacter, Lee
;  TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in H
;  FILE REFERENCE: 10739-1
;  CURRENT APPLICATION NUMBER: US/10/072,419
;  CURRENT FILING DATE:  2002-02-07
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Vanessa cardui
US-10-072-419-37

  Query Match             85.0%;  Score 17;  DB 24;  Length 11;
  Best Local Similarity   40.0%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      4 FTSSW 8


RESULT 7
US-09-355-397C-36
; Sequence 36, Application US/09355397C
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; GENERAL INFORMATION:
;  APPLICANT: Spyrou, Giannis
;  TITLE OF INVENTION: Mammalian Thioredoxin
;  FILE REFERENCE: 102043-100
;  CURRENT APPLICATION NUMBER: US/09/355,397C
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: PCT/GB98/00263
;  PRIOR FILING DATE: 1998-01-28
;  PRIOR APPLICATION NUMBER: GB 9701710.7
;  PRIOR FILING DATE: 1997-01-28
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: mammal
US-09-355-397C-36

  Query Match             85.0%;  Score 17;  DB 17;  Length 14;
  Best Local Similarity   40.0%;  Pred. No. 2e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       5 FSATW 9


RESULT 8
US-09-308-027-12
; Sequence 12, Application US/09308027
; GENERAL INFORMATION:
;  APPLICANT:  Sone, Toshio
;  APPLICANT:  Kume, Akinori
;  APPLICANT:  Dairiki, Kazuo
;  APPLICANT:  Kino, Koshuke
;  TITLE OF INVENTION:  PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
;  FILE REFERENCE:  06501/031001
;  CURRENT APPLICATION NUMBER: US/09/308,027
;  CURRENT FILING DATE:  1999-08-16
;  PRIOR APPLICATION NUMBER:  PCT/JP97/04129
;  PRIOR FILING DATE:  1997-11-12
;  PRIOR APPLICATION NUMBER:  JP 8/302053
;  PRIOR FILING DATE:  1996-11-13
;  NUMBER OF SEQ ID NOS:  146
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Cryptomeria
US-09-308-027-12

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       9 FSTAW 13


RESULT 9
US-09-308-027-88
; Sequence 88, Application US/09308027
; GENERAL INFORMATION:
;  APPLICANT:  Sone, Toshio
;  APPLICANT:  Kume, Akinori
;  APPLICANT:  Dairiki, Kazuo
;  APPLICANT:  Kino, Koshuke
;  TITLE OF INVENTION:  PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
;  FILE REFERENCE:  06501/031001
;  CURRENT APPLICATION NUMBER: US/09/308,027
;  CURRENT FILING DATE:  1999-08-16
;  PRIOR APPLICATION NUMBER:  PCT/JP97/04129
;  PRIOR FILING DATE:  1997-11-12
;  PRIOR APPLICATION NUMBER:  JP 8/302053
;  PRIOR FILING DATE:  1996-11-13
;  NUMBER OF SEQ ID NOS:  146
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 88
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Cryptomeria
US-09-308-027-88

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSTAW 8


RESULT 10
US-09-308-027A-12
; Sequence 12, Application US/09308027A
; GENERAL INFORMATION:
;  APPLICANT: Sone, Toshio
;  APPLICANT:  Kume, Akinori
;  APPLICANT:  Dairiki, Kazuo
;  APPLICANT:  Kino, Kohsuke
;  TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
;  FILE REFERENCE: 06501/031001
;  CURRENT APPLICATION NUMBER: US/09/308,027A
;  CURRENT FILING DATE:  1999-08-16
;  PRIOR APPLICATION NUMBER: PCT/JP97/04129
;  PRIOR FILING DATE: 1997-11-12
;  PRIOR APPLICATION NUMBER: JP 8/302053
;  PRIOR FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Cryptomeria
US-09-308-027A-12

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       9 FSTAW 13


RESULT 11
US-09-308-027A-88
; Sequence 88, Application US/09308027A
; GENERAL INFORMATION:
;  APPLICANT: Sone, Toshio
;  APPLICANT:  Kume, Akinori
;  APPLICANT:  Dairiki, Kazuo
;  APPLICANT:  Kino, Kohsuke
;  TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
;  FILE REFERENCE: 06501/031001
;  CURRENT APPLICATION NUMBER: US/09/308,027A
;  CURRENT FILING DATE:  1999-08-16
;  PRIOR APPLICATION NUMBER: PCT/JP97/04129
;  PRIOR FILING DATE: 1997-11-12
;  PRIOR APPLICATION NUMBER: JP 8/302053
;  PRIOR FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 88
;   LENGTH: 15
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;   TYPE: PRT
;   ORGANISM: Cryptomeria
US-09-308-027A-88

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSTAW 8


RESULT 12
US-09-963-339-10
; Sequence 10, Application US/09963339
; GENERAL INFORMATION:
;  APPLICANT: Bandaru, Rajasekhar
;  TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
;  TITLE OF INVENTION:  FAMILY MEMBERS AND USES THEREOF
;  FILE REFERENCE: 10448-090001
;  CURRENT APPLICATION NUMBER: US/09/963,339
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 60/235,049
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-963-339-10

  Query Match             85.0%;  Score 17;  DB 23;  Length 19;
  Best Local Similarity   40.0%;  Pred. No. 2.4e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSATW 8


RESULT 13
US-10-145-586-59
; Sequence 59, Application US/10145586
; GENERAL INFORMATION:
;  APPLICANT: Alexandra Glucksmann, Maria
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  M. Galvin, Katherine
;  APPLICANT:  Weich, Nadine
;  APPLICANT:  Curtis, Rory A.J.
;  APPLICANT:  Bandaru, Rajasekhar
;  APPLICANT:  Kapeller-Libermann, Rosana
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
;  TITLE OF INVENTION:  HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
;  TITLE OF INVENTION:  REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
;  FILE REFERENCE: 10448-188001
;  CURRENT APPLICATION NUMBER: US/10/145,586
;  CURRENT FILING DATE:  2002-05-14
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 95
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-145-586-59

  Query Match             85.0%;  Score 17;  DB 25;  Length 19;
  Best Local Similarity   40.0%;  Pred. No. 2.4e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSATW 8


RESULT 14
US-09-202-464-45
; Sequence 45, Application US/09202464
;   GENERAL INFORMATION:
;        APPLICANT: Kino, Kohsuke
;                   Dairiki, Kazuo
;        TITLE OF INVENTION: T-CELL EPITOPE PEPTIDES
;        NUMBER OF SEQUENCES: 90
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 225 Franklin Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02110-2804
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/202,464
;             FILING DATE: 14-Dec-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: WO JP97/02031
;             FILING DATE: 12-JUN-1997
;             APPLICATION NUMBER: JP 8/153527
;             FILING DATE: 14-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fraser, Ph.D., J.D., Janis K.
;             REGISTRATION NUMBER: 34,819
;             REFERENCE/DOCKET NUMBER: 06501-024001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617/542-5070
;             TELEFAX: 617/542-8906
;   INFORMATION FOR SEQ ID NO: 45:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-202-464-45

  Query Match             85.0%;  Score 17;  DB 16;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       8 FATTW 12


RESULT 15
US-09-240-203B-265
; Sequence 265, Application US/09240203B
;   GENERAL INFORMATION:
;        APPLICANT: Griffith, Irwin J.;
;                   Pollock, Joanne;
;                   Bond, Julian F.;
;                   Garman, Richard D;
;                   Kuo, Mei-Chang;
;                   Powers, Steven P.;
;                   Exley, Mark A.;
;                   Chen, Xian;
;                   Shaked, Ze'ev
;        TITLE OF INVENTION: Allergenic Proteins And Peptides From
;                            Japanese Cedar Pollen
;        NUMBER OF SEQUENCES: 265
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;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lahive & Cockfield, LLP
;             STREET: 28 State St
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/240,203B
;             FILING DATE: 22-Jun-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/350,225
;             FILING DATE: December 6, 1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amy E. Mandragouras, Esq.
;             REGISTRATION NUMBER: 36,207
;             REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617) 227-7400
;             TELEFAX: (617) 742-4214
;   INFORMATION FOR SEQ ID NO: 265:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        FRAGMENT TYPE: internal
;        SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-240-203B-265

  Query Match             85.0%;  Score 17;  DB 16;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      12 FSTAW 16


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Sequence: 1 FXXXW 5

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Post-processing: Minimum Match 0%
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
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4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	41	5	US-09-966-264D-41	Sequence 41, Appl
2	17	85.0	44	6	US-10-203-138A-12357	Sequence 12357, A
3	17	85.0	46	6	US-10-203-138A-12178	Sequence 12178, A
4	17	85.0	51	1	PCT-US02-32727-19679	Sequence 19679, A
5	17	85.0	51	6	US-10-057-498-19679	Sequence 19679, A
6	17	85.0	52	1	PCT-US02-32727-17963	Sequence 17963, A
7	17	85.0	52	6	US-10-057-498-17963	Sequence 17963, A
8	17	85.0	54	5	US-09-733-643B-21	Sequence 21, Appl
9	17	85.0	56	1	PCT-US02-32727-25901	Sequence 25901, A
10	17	85.0	56	6	US-10-057-498-25901	Sequence 25901, A
11	17	85.0	58	1	PCT-US02-32727-8139	Sequence 8139, Ap
12	17	85.0	58	6	US-10-057-498-8139	Sequence 8139, Ap
13	17	85.0	60	1	PCT-US02-32727-26135	Sequence 26135, A
14	17	85.0	60	6	US-10-057-498-26135	Sequence 26135, A
15	17	85.0	61	1	PCT-US02-32727-7101	Sequence 7101, Ap
16	17	85.0	61	6	US-10-092-411A-4258	Sequence 4258, Ap
17	17	85.0	61	6	US-10-057-498-7101	Sequence 7101, Ap
18	17	85.0	63	1	PCT-US02-32727-3486	Sequence 3486, Ap
19	17	85.0	63	6	US-10-057-498-3486	Sequence 3486, Ap
20	17	85.0	67	1	PCT-US02-32727-3015	Sequence 3015, Ap
21	17	85.0	67	6	US-10-057-498-3015	Sequence 3015, Ap
22	17	85.0	68	1	PCT-US02-32727-4894	Sequence 4894, Ap
23	17	85.0	68	6	US-10-057-498-4894	Sequence 4894, Ap
24	17	85.0	69	1	PCT-US02-32727-13373	Sequence 13373, A
25	17	85.0	69	6	US-10-057-498-13373	Sequence 13373, A
26	17	85.0	71	1	PCT-US02-32727-8519	Sequence 8519, Ap
27	17	85.0	71	6	US-10-057-498-8519	Sequence 8519, Ap
28	17	85.0	72	1	PCT-US02-32727-9882	Sequence 9882, Ap
29	17	85.0	72	6	US-10-057-498-9882	Sequence 9882, Ap
30	17	85.0	74	1	PCT-US02-32727-16040	Sequence 16040, A
31	17	85.0	74	1	PCT-US02-32727-28942	Sequence 28942, A
32	17	85.0	74	6	US-10-057-498-16040	Sequence 16040, A
33	17	85.0	74	6	US-10-057-498-28942	Sequence 28942, A
34	17	85.0	76	1	PCT-US02-32727-848	Sequence 848, App
35	17	85.0	76	1	PCT-US02-32727-30499	Sequence 30499, A
36	17	85.0	76	6	US-10-057-498-848	Sequence 848, App
37	17	85.0	78	5	US-09-724-676-63184	Sequence 63184, A
38	17	85.0	78	5	US-09-724-676A-63184	Sequence 63184, A
39	17	85.0	78	6	US-10-203-138A-10907	Sequence 10907, A
40	17	85.0	82	5	US-09-950-084-5109	Sequence 5109, Ap
41	17	85.0	83	6	US-10-218-140-866	Sequence 866, App
42	17	85.0	85	1	PCT-US02-32727-11518	Sequence 11518, A
43	17	85.0	85	6	US-10-057-498-11518	Sequence 11518, A
44	17	85.0	86	1	PCT-US02-32727-25616	Sequence 25616, A
45	17	85.0	86	6	US-10-057-498-25616	Sequence 25616, A

ALIGNMENTS

RESULT 1
US-09-966-264D-41
; Sequence 41, Application US/09966264D
; GENERAL INFORMATION:
; APPLICANT: Barber, Elizabeth K
; TITLE OF INVENTION: Gene Expression Control Element DNA
; FILE REFERENCE: 896034605001
; CURRENT APPLICATION NUMBER: US/09/966,264D
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/237,079
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 41
; TYPE: PRT
; ORGANISM: human
US-09-966-264D-41

Query Match 85.0%; Score 17; DB 5; Length 41;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 2 FASSW 6

RESULT 2
US-10-203-138A-12357
; Sequence 12357, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6

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;  PRIOR FILING DATE: 03 October 2000 (03.10.00)
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 27 September 2000 (27.09.00)
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 21 September 2000 (21.09.00)
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 30 June 2000 (30.06.00)
;  NUMBER OF SEQ ID NOS: 15438
;  SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 12357
;   LENGTH: 44
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC004852.2
;   FEATURE:
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
;   FEATURE:
;   OTHER INFORMATION: EST_HUMAN HIT: AA320774.1, EVALUE 5.00e-10
;   FEATURE:
;   OTHER INFORMATION: SWISSPROT HIT: P11369, EVALUE 1.00e-03
US-10-203-138A-12357

  Query Match             85.0%;  Score 17;  DB 6;  Length 44;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      18 FAATW 22


RESULT 3
US-10-203-138A-12178
; Sequence 12178, Application US/10203138A
; GENERAL INFORMATION:
;  APPLICANT: Molecular Dynamics, Inc.
;  APPLICANT:  Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  ANALYSIS OF GENE EXPRESSION IN BT 474
;  FILE REFERENCE: PB 0004 WO 8
;  CURRENT APPLICATION NUMBER: US/10/203,138A
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 04 February 2000 (04.02.00)
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 26 May 2000 (26.05.00)
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 03 August 2000 (03.08.00)
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 03 October 2000 (03.10.00)
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 27 September 2000 (27.09.00)
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 21 September 2000 (21.09.00)
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 30 June 2000 (30.06.00)
;  NUMBER OF SEQ ID NOS: 15438
;  SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 12178
;   LENGTH: 46
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC007938.1
;   FEATURE:
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.7
;   FEATURE:
;   OTHER INFORMATION: EST_HUMAN HIT: BF642802.1, EVALUE 2.00e-19
;   FEATURE:
;   OTHER INFORMATION: SWISSPROT HIT: P53620, EVALUE 5.00e-15
US-10-203-138A-12178

  Query Match             85.0%;  Score 17;  DB 6;  Length 46;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      20 FAAAW 24


RESULT 4
PCT-US02-32727-19679
; Sequence 19679, Application PC/TUS0232727
; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Persing, David
;  APPLICANT:  Bhatia, Ajay
;  APPLICANT:  Maisonneuve, Jean Francois
;  APPLICANT:  Zhang, Yanni
;  APPLICANT:  Wang, Siqing
;  APPLICANT:  Jen, Shyian
;  APPLICANT:  Lodes, Michael
;  APPLICANT:  Benson, Darin
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Barth, Brenda
;  APPLICANT:  Douglass,John
;  TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
;  FILE REFERENCE: 210121.514C1
;  CURRENT APPLICATION NUMBER: PCT/US02/32727
;  CURRENT FILING DATE:  2002-10-11
;  NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 19679
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Propioni acnes
PCT-US02-32727-19679

  Query Match             85.0%;  Score 17;  DB 1;  Length 51;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      33 FASSW 37


RESULT 5
US-10-057-498-19679
; Sequence 19679, Application US/10057498
; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Persing, David
;  TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
;  FILE REFERENCE: 210121.514
;  CURRENT APPLICATION NUMBER: US/10/057,498
;  CURRENT FILING DATE:  2001-04-20
;  NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 19679
;   LENGTH: 51
;   TYPE: PRT
;   ORGANISM: Propioni acnes
US-10-057-498-19679

  Query Match             85.0%;  Score 17;  DB 6;  Length 51;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
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```
          |   |
Db      33 FASSW 37


RESULT 6
PCT-US02-32727-17963
; Sequence 17963, Application PC/TUS0232727
; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Persing, David
;  APPLICANT:  Bhatia, Ajay
;  APPLICANT:  Maisonneuve, Jean Francois
;  APPLICANT:  Zhang, Yanni
;  APPLICANT:  Wang, Siqing
;  APPLICANT:  Jen, Shyian
;  APPLICANT:  Lodes, Michael
;  APPLICANT:  Benson, Darin
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Barth, Brenda
;  APPLICANT:  Douglass,John
;  TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes V
;  FILE REFERENCE: 210121.514C1
;  CURRENT APPLICATION NUMBER: PCT/US02/32727
;  CURRENT FILING DATE:  2002-10-11
;  NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 17963
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Propioni acnes
PCT-US02-32727-17963

  Query Match             85.0%;  Score 17;  DB 1;  Length 52;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       8 FSSSW 12


RESULT 7
US-10-057-498-17963
; Sequence 17963, Application US/10057498
; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Persing, David
;  TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes V
;  FILE REFERENCE: 210121.514
;  CURRENT APPLICATION NUMBER: US/10/057,498
;  CURRENT FILING DATE:  2001-04-20
;  NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 17963
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Propioni acnes
US-10-057-498-17963

  Query Match             85.0%;  Score 17;  DB 6;  Length 52;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       8 FSSSW 12


RESULT 8
US-09-733-643B-21
; Sequence 21, Application US/09733643B
; GENERAL INFORMATION:
;  APPLICANT: Laroche, Andre J.
;  APPLICANT:  Huang, Timothy Y
;  APPLICANT:  Lu, Zhen-Xiang
;  APPLICANT:  Frick, Michele M.
;  APPLICANT:  Huang, Hung Chang
;  APPLICANT:  Cheng, Kuo Joan
;  TITLE OF INVENTION: Coniothyrium minitans beta-(1,3) exoglucanase gene
;  TITLE OF INVENTION:  cbeg1
;  FILE REFERENCE: 24014US1
;  CURRENT APPLICATION NUMBER: US/09/733,643B
;  CURRENT FILING DATE:  2000-12-08
;  PRIOR APPLICATION NUMBER: US 60/170,168
;  PRIOR FILING DATE: 1999-12-12
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 54
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   OTHER INFORMATION: Exopg
US-09-733-643B-21

  Query Match             85.0%;  Score 17;  DB 5;  Length 54;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      23 FAAAW 27


RESULT 9
PCT-US02-32727-25901
; Sequence 25901, Application PC/TUS0232727
; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Persing, David
;  APPLICANT:  Bhatia, Ajay
;  APPLICANT:  Maisonneuve, Jean Francois
;  APPLICANT:  Zhang, Yanni
;  APPLICANT:  Wang, Siqing
;  APPLICANT:  Jen, Shyian
;  APPLICANT:  Lodes, Michael
;  APPLICANT:  Benson, Darin
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Barth, Brenda
;  APPLICANT:  Douglass,John
;  TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
;  FILE REFERENCE: 210121.514C1
;  CURRENT APPLICATION NUMBER: PCT/US02/32727
;  CURRENT FILING DATE:  2002-10-11
;  NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 25901
;   LENGTH: 56
;   TYPE: PRT
;   ORGANISM: Propioni acnes
PCT-US02-32727-25901

  Query Match             85.0%;  Score 17;  DB 1;  Length 56;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      45 FTSTW 49


RESULT 10
US-10-057-498-25901
; Sequence 25901, Application US/10057498
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; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Persing, David
;  TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes V
;  FILE REFERENCE: 210121.514
;  CURRENT APPLICATION NUMBER: US/10/057,498
;  CURRENT FILING DATE:  2001-04-20
;  NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 25901
;   LENGTH: 56
;   TYPE: PRT
;   ORGANISM: Propioni acnes
US-10-057-498-25901

  Query Match             85.0%;  Score 17;  DB 6;  Length 56;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      45 FTSTW 49


RESULT 11
PCT-US02-32727-8139
; Sequence 8139, Application PC/TUS0232727
; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Persing, David
;  APPLICANT:  Bhatia, Ajay
;  APPLICANT:  Maisonneuve, Jean Francois
;  APPLICANT:  Zhang, Yanni
;  APPLICANT:  Wang, Siqing
;  APPLICANT:  Jen, Shyian
;  APPLICANT:  Lodes, Michael
;  APPLICANT:  Benson, Darin
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Barth, Brenda
;  APPLICANT:  Douglass,John
;  TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes V
;  FILE REFERENCE: 210121.514C1
;  CURRENT APPLICATION NUMBER: PCT/US02/32727
;  CURRENT FILING DATE:  2002-10-11
;  NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 8139
;   LENGTH: 58
;   TYPE: PRT
;   ORGANISM: Propioni acnes
PCT-US02-32727-8139

  Query Match             85.0%;  Score 17;  DB 1;  Length 58;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      45 FATSW 49


RESULT 12
US-10-057-498-8139
; Sequence 8139, Application US/10057498
; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Persing, David
;  TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes V
;  FILE REFERENCE: 210121.514
;  CURRENT APPLICATION NUMBER: US/10/057,498
;  CURRENT FILING DATE:  2001-04-20
;  NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 8139
;   LENGTH: 58
;   TYPE: PRT
;   ORGANISM: Propioni acnes
US-10-057-498-8139

  Query Match             85.0%;  Score 17;  DB 6;  Length 58;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      45 FATSW 49


RESULT 13
PCT-US02-32727-26135
; Sequence 26135, Application PC/TUS0232727
; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Persing, David
;  APPLICANT:  Bhatia, Ajay
;  APPLICANT:  Maisonneuve, Jean Francois
;  APPLICANT:  Zhang, Yanni
;  APPLICANT:  Wang, Siqing
;  APPLICANT:  Jen, Shyian
;  APPLICANT:  Lodes, Michael
;  APPLICANT:  Benson, Darin
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Barth, Brenda
;  APPLICANT:  Douglass,John
;  TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
;  FILE REFERENCE: 210121.514C1
;  CURRENT APPLICATION NUMBER: PCT/US02/32727
;  CURRENT FILING DATE:  2002-10-11
;  NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 26135
;   LENGTH: 60
;   TYPE: PRT
;   ORGANISM: Propioni acnes
PCT-US02-32727-26135

  Query Match             85.0%;  Score 17;  DB 1;  Length 60;
  Best Local Similarity   40.0%;  Pred. No. 2.3e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      34 FSTTW 38


RESULT 14
US-10-057-498-26135
; Sequence 26135, Application US/10057498
; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Persing, David
;  TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
;  FILE REFERENCE: 210121.514
;  CURRENT APPLICATION NUMBER: US/10/057,498
;  CURRENT FILING DATE:  2001-04-20
;  NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 26135
;   LENGTH: 60
;   TYPE: PRT
;   ORGANISM: Propioni acnes
US-10-057-498-26135

  Query Match             85.0%;  Score 17;  DB 6;  Length 60;
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  Best Local Similarity   40.0%;  Pred. No. 2.3e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      34 FSTTW 38


RESULT 15
PCT-US02-32727-7101
; Sequence 7101, Application PC/TUS0232727
; GENERAL INFORMATION:
;  APPLICANT: Mitcham, Jennifer
;  APPLICANT:  Skeiky, Yasir
;  APPLICANT:  Persing, David
;  APPLICANT:  Bhatia, Ajay
;  APPLICANT:  Maisonneuve, Jean Francois
;  APPLICANT:  Zhang, Yanni
;  APPLICANT:  Wang, Siqing
;  APPLICANT:  Jen, Shyian
;  APPLICANT:  Lodes, Michael
;  APPLICANT:  Benson, Darin
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Barth, Brenda
;  APPLICANT:  Douglass,John
;  TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes V
;  FILE REFERENCE: 210121.514C1
;  CURRENT APPLICATION NUMBER: PCT/US02/32727
;  CURRENT FILING DATE:  2002-10-11
;  NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 7101
;   LENGTH: 61
;   TYPE: PRT
;   ORGANISM: Propioni acnes
PCT-US02-32727-7101

  Query Match            85.0%;  Score 17;  DB 1;  Length 61;
  Best Local Similarity   40.0%;  Pred. No. 2.3e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      22 FSSSW 26


Search completed: January 29, 2003, 14:15:47
Job time : 18 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:10:42 ; Search time 15 Seconds
(without alignments)
9.808 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	13	4	US-09-085-072-7	Sequence 7, Appli
2	17	85.0	29	4	US-08-469-260A-428	Sequence 428, App
3	17	85.0	34	1	US-08-118-270-134	Sequence 134, App
4	17	85.0	34	1	US-08-118-270-172	Sequence 172, App
5	17	85.0	34	5	PCT-US93-08528-134	Sequence 134, App
6	17	85.0	34	5	PCT-US93-08528-172	Sequence 172, App
7	17	85.0	36	3	US-08-467-023-137	Sequence 137, App
8	17	85.0	37	4	US-09-330-914A-10	Sequence 10, Appl
9	17	85.0	41	3	US-08-467-023-136	Sequence 136, App
10	17	85.0	45	3	US-08-467-023-135	Sequence 135, App
11	17	85.0	45	4	US-09-149-476-475	Sequence 475, App
12	17	85.0	49	1	US-08-118-270-209	Sequence 209, App
13	17	85.0	49	5	PCT-US93-08528-209	Sequence 209, App
14	17	85.0	61	4	US-09-134-001C-4258	Sequence 4258, Ap
15	17	85.0	80	4	US-09-330-914A-4	Sequence 4, Appli
16	17	85.0	84	2	US-08-353-476-78	Sequence 78, Appl
17	17	85.0	84	4	US-08-679-493A-97	Sequence 97, Appl
18	17	85.0	91	2	US-08-598-873-19	Sequence 19, Appl
19	17	85.0	91	4	US-08-605-430-19	Sequence 19, Appl
20	17	85.0	102	3	US-08-984-295-3	Sequence 3, Appli
21	17	85.0	102	3	US-08-741-411-12	Sequence 12, Appl
22	17	85.0	104	6	5210073-1	Patent No. 5210073
23	17	85.0	105	2	US-08-826-910-3	Sequence 3, Appli
24	17	85.0	105	2	US-08-826-910-4	Sequence 4, Appli
25	17	85.0	114	4	US-09-450-520A-9	Sequence 9, Appli
26	17	85.0	114	4	US-09-450-520A-10	Sequence 10, Appl
27	17	85.0	114	4	US-09-450-520A-11	Sequence 11, Appl
28	17	85.0	116	3	US-09-065-059-9	Sequence 9, Appli
29	17	85.0	116	3	US-08-545-809A-134	Sequence 134, App
30	17	85.0	117	1	US-07-634-278-105	Sequence 105, App
31	17	85.0	117	1	US-08-477-728-105	Sequence 105, App
32	17	85.0	117	1	US-08-474-040-105	Sequence 105, App
33	17	85.0	117	1	US-08-487-200-105	Sequence 105, App
34	17	85.0	117	4	US-08-484-537-105	Sequence 105, App
35	17	85.0	120	3	US-09-065-059-1	Sequence 1, Appli
36	17	85.0	122	4	US-09-540-014-2	Sequence 2, Appli
37	17	85.0	127	4	US-09-540-014-4	Sequence 4, Appli
38	17	85.0	128	3	US-08-467-023-187	Sequence 187, App
39	17	85.0	130	1	US-08-276-852-69	Sequence 69, Appl
40	17	85.0	130	1	US-08-276-852-70	Sequence 70, Appl
41	17	85.0	130	1	US-08-276-852-71	Sequence 71, Appl
42	17	85.0	130	1	US-08-899-575-69	Sequence 69, Appl
43	17	85.0	130	1	US-08-899-575-70	Sequence 70, Appl
44	17	85.0	130	1	US-08-899-575-71	Sequence 71, Appl
45	17	85.0	130	1	US-08-899-575-69	Sequence 69, Appl

ALIGNMENTS

```
RESULT 1
US-09-085-072-7
; Sequence 7, Application US/09085072
; Patent No. 6265150
;  GENERAL INFORMATION:
;    APPLICANT:  L. Terstappen et al.
;    TITLE OF INVENTION:  PHAGE ANTIBODIES
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann & Baron, LLP
;      STREET:  350 Jericho Turnpike
;      CITY:  Jericho
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11753
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/085,072
;      FILING DATE:  26-MAY-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Feit, Irving N.
;      REGISTRATION NUMBER:  28,601
;      REFERENCE/DOCKET NUMBER:  890-2 FWC/CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 822-3550
;      TELEFAX:  (516) 822-3582
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-085-072-7

  Query Match             85.0%;  Score 17;  DB 4;  Length 13;
  Best Local Similarity   40.0%;  Pred. No. 8.7e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       6 FASSW 10


RESULT 2
```

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US-08-469-260A-428
; Sequence 428, Application US/08469260A
; Patent No. 6451578
;  GENERAL INFORMATION:
;    APPLICANT:  JOHN N. SIMONS
;    APPLICANT:  TAMI J. PILOT-MATIAS
;    APPLICANT:  GEORGE J. DAWSON
;    APPLICANT:  GEORGE G. SCHLAUDER
;    APPLICANT:  SURESH M. DESAI
;    APPLICANT:  THOMAS P. LEARY
;    APPLICANT:  ANTHONY SCOTT MUERHOFF
;    APPLICANT:  JAMES C. ERKER
;    APPLICANT:  SHERI L. BUIJK
;    APPLICANT:  ISA K. MUSHAHWAR
;    TITLE OF INVENTION:  NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
;    TITLE OF INVENTION:  REAGENTS AND METHODS FOR THEIR USE
;    NUMBER OF SEQUENCES:  716
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ABBOTT LABORATORIES  D377/AP6D
;      STREET:  100 ABBOTT PARK ROAD
;      CITY:  ABBOTT PARK
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,260A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/424,550
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  POREMBSKI, PRISCILLA E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5527.PC.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-6365
;      TELEFAX:  708-938-2623
;  INFORMATION FOR SEQ ID NO:  428:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-469-260A-428

  Query Match             85.0%;  Score 17;  DB 4;  Length 29;
  Best Local Similarity   40.0%;  Pred. No. 1.5e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      12 FASAW 16


RESULT 3
US-08-118-270-134
; Sequence 134, Application US/08118270
; Patent No. 5508384
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Randall B.
;    APPLICANT:  Schuster, David I.
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,270
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  134:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-118-270-134

  Query Match             85.0%;  Score 17;  DB 1;  Length 34;
  Best Local Similarity   40.0%;  Pred. No. 1.7e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      16 FTSAW 20


RESULT 4
US-08-118-270-172
; Sequence 172, Application US/08118270
; Patent No. 5508384
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Randall B.
;    APPLICANT:  Schuster, David I.
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,270
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2A
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  172:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-118-270-172

  Query Match             85.0%;  Score 17;  DB 1;  Length 34;
  Best Local Similarity   40.0%;  Pred. No. 1.7e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      16 FTTAW 20


RESULT 5
PCT-US93-08528-134
; Sequence 134, Application PC/TUS9308528
;  GENERAL INFORMATION:
;    APPLICANT:  New York University
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08528
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  134:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-08528-134

  Query Match             85.0%;  Score 17;  DB 5;  Length 34;
  Best Local Similarity   40.0%;  Pred. No. 1.7e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      16 FTSAW 20


RESULT 6
PCT-US93-08528-172
; Sequence 172, Application PC/TUS9308528
;  GENERAL INFORMATION:
;    APPLICANT:  New York University
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08528
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  172:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-08528-172

  Query Match             85.0%;  Score 17;  DB 5;  Length 34;
  Best Local Similarity   40.0%;  Pred. No. 1.7e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      16 FTTAW 20


RESULT 7
US-08-467-023-137
; Sequence 137, Application US/08467023
; Patent No. 6090386
;  GENERAL INFORMATION:
;    APPLICANT:  Griffeth, Irwin J.;
;    APPLICANT:  Pollock, Joanne;
;    APPLICANT:  Bond, Julian F.;
;    APPLICANT:  Garman, Richard D;
;    APPLICANT:  Kuo, Mei-Chang;
;    APPLICANT:  Yeung, Siu-mei H.;
;    APPLICANT:  Brauer, Andrew;
;    APPLICANT:  Exley, Mark A.;
;    APPLICANT:  Powers, Steven P.
;    TITLE OF INVENTION:  Allergenic Proteins And Peptides From
;    TITLE OF INVENTION:  Japanese Cedar Pollen
;    NUMBER OF SEQUENCES:  261
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ImmuLogic Pharmaceutical Corporation, Inc.
;      STREET:  610 Lincoln St
```

```
;       CITY:  Waltham
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02154
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/467,023
;       FILING DATE:  June 6, 1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/350,225
;       FILING DATE:  December 6, 1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jane E. Remillard
;       REGISTRATION NUMBER:  38,872
;       REFERENCE/DOCKET NUMBER:  025.6 USD2 (IMI-028CPD2)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 227-7400
;       TELEFAX:  (617) 227-5941
;   INFORMATION FOR SEQ ID NO:  137:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  36 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal
US-08-467-023-137

  Query Match             85.0%;  Score 17;  DB 3;  Length 36;
  Best Local Similarity   40.0%;  Pred. No. 1.8e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      28 FSTAW 32


RESULT 8
US-09-330-914A-10
; Sequence 10, Application US/09330914A
; Patent No. 6432671
;   GENERAL INFORMATION:
;         APPLICANT: Flohe, Leopold
;                    No. 6432671eceke, Everson
;                    Kalisz, Henryk
;                    Montemartini, Marisa
;         TITLE OF INVENTION: TRYPAREDOXIN, EXPRESSION PLASMID, PROCESS OF
;                             PRODUCTION,    METHOD OF USE, TEST KIT, AND
;                             PHARMACEUTICAL COMPOSITION
;         NUMBER OF SEQUENCES: 15
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun
;              STREET: 233 South Wacker Drive/6300 Sears Tower
;              CITY: Chicago
;              STATE: Illinois
;              COUNTRY: Unites States of America
;              ZIP: 60606
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/330,914A
;              FILING DATE: 11-Jun-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: WO PCT/EP97/06983
;              FILING DATE: 12-DEC-1997
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Zeller, James P.
;              REGISTRATION NUMBER: 28,491
;              REFERENCE/DOCKET NUMBER: 29473/35678
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (312) 474-6300
;              TELEFAX: (312) 474-0448
;    INFORMATION FOR SEQ ID NO: 10:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 37 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: peptide
;         HYPOTHETICAL: NO
;         ANTI-SENSE: NO
;         SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-330-914A-10

  Query Match             85.0%;  Score 17;  DB 4;  Length 37;
  Best Local Similarity   40.0%;  Pred. No. 1.8e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      11 FSASW 15


RESULT 9
US-08-467-023-136
; Sequence 136, Application US/08467023
; Patent No. 6090386
;  GENERAL INFORMATION:
;    APPLICANT:  Griffeth, Irwin J.;
;    APPLICANT:  Pollock, Joanne;
;    APPLICANT:  Bond, Julian F.;
;    APPLICANT:  Garman, Richard D;
;    APPLICANT:  Kuo, Mei-Chang;
;    APPLICANT:  Yeung, Siu-mei H.;
;    APPLICANT:  Brauer, Andrew;
;    APPLICANT:  Exley, Mark A.;
;    APPLICANT:  Powers, Steven P.
;    TITLE OF INVENTION:  Allergenic Proteins And Peptides From
;    TITLE OF INVENTION:  Japanese Cedar Pollen
;    NUMBER OF SEQUENCES:  261
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ImmuLogic Pharmaceutical Corporation, Inc.
;      STREET:  610 Lincoln St
;      CITY:  Waltham
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,023
;      FILING DATE:  June 6, 1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/350,225
;      FILING DATE:  December 6, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane E. Remillard
;      REGISTRATION NUMBER:  38,872
;      REFERENCE/DOCKET NUMBER:  025.6 USD2 (IMI-028CPD2)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  136:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  41 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-467-023-136

  Query Match             85.0%;  Score 17;  DB 3;  Length 41;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      33 FSTAW 37


RESULT 10
US-08-467-023-135
; Sequence 135, Application US/08467023
; Patent No. 6090386
;  GENERAL INFORMATION:
;    APPLICANT:  Griffeth, Irwin J.;
;    APPLICANT:  Pollock, Joanne;
;    APPLICANT:  Bond, Julian F.;
;    APPLICANT:  Garman, Richard D;
;    APPLICANT:  Kuo, Mei-Chang;
;    APPLICANT:  Yeung, Siu-mei H.;
;    APPLICANT:  Brauer, Andrew;
;    APPLICANT:  Exley, Mark A.;
;    APPLICANT:  Powers, Steven P.
;    TITLE OF INVENTION:  Allergenic Proteins And Peptides From
;    TITLE OF INVENTION:  Japanese Cedar Pollen
;    NUMBER OF SEQUENCES:  261
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ImmuLogic Pharmaceutical Corporation, Inc.
;      STREET:  610 Lincoln St
;      CITY:  Waltham
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,023
;      FILING DATE:  June 6, 1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/350,225
;      FILING DATE:  December 6, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane E. Remillard
;      REGISTRATION NUMBER:  38,872
;      REFERENCE/DOCKET NUMBER:  025.6 USD2 (IM1-028CPD2)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  135:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-467-023-135

  Query Match             85.0%;  Score 17;  DB 3;  Length 45;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      33 FSTAW 37


RESULT 11
US-09-149-476-475
; Sequence 475, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/038,621
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,626
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,334
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,336
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,163
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/047,600
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,615
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,597
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,502
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,633
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,583
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,617
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,618
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,503
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,592
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,581
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,584
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,500
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,587
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,492
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,598
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,613
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,582
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,596
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,612
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,632
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,601
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
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; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 85.0%; Score 17; DB 4; Length 45;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1 FXXXW 5
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Db      31 FSAAW 35
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RESULT 12
US-08-118-270-209
; Sequence 209, Application US/08118270

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; Patent No. 5508384
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Randall B.
;    APPLICANT:  Schuster, David I.
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,270
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  209:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  49 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-118-270-209

  Query Match             85.0%;  Score 17;  DB 1;  Length 49;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      36 FTSAW 40


RESULT 13
PCT-US93-08528-209
; Sequence 209, Application PC/TUS9308528
;  GENERAL INFORMATION:
;    APPLICANT:  New York University
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08528
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  209:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  49 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-08528-209

  Query Match             85.0%;  Score 17;  DB 5;  Length 49;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      36 FTSAW 40


RESULT 14
US-09-134-001C-4258
; Sequence 4258, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4258
;   LENGTH: 61
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4258

  Query Match             85.0%;  Score 17;  DB 4;  Length 61;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      14 FSTSW 18


RESULT 15
US-09-330-914A-4
; Sequence 4, Application US/09330914A
; Patent No. 6432671
;   GENERAL INFORMATION:
;        APPLICANT: Flohe, Leopold
;                   No. 6432671eceke, Everson
;                   Kalisz, Henryk
;                   Montemartini, Marisa
;        TITLE OF INVENTION: TRYPAREDOXIN, EXPRESSION PLASMID, PROCESS OF
;                            PRODUCTION,    METHOD OF USE, TEST KIT, AND
;                            PHARMACEUTICAL COMPOSITION
;
```

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;         NUMBER OF SEQUENCES: 15
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun
;              STREET: 233 South Wacker Drive/6300 Sears Tower
;              CITY: Chicago
;              STATE: Illinois
;              COUNTRY: Unites States of America
;              ZIP: 60606
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/330,914A
;              FILING DATE: 11-Jun-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: WO PCT/EP97/06983
;              FILING DATE: 12-DEC-1997
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Zeller, James P.
;              REGISTRATION NUMBER: 28,491
;              REFERENCE/DOCKET NUMBER: 29473/35678
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (312) 474-6300
;              TELEFAX: (312) 474-0448
;    INFORMATION FOR SEQ ID NO: 4:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 80 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         HYPOTHETICAL: NO
;         ANTI-SENSE: NO
;         SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-330-914A-4

  Query Match             85.0%;  Score 17;  DB 4;  Length 80;
  Best Local Similarity   40.0%;  Pred. No. 3.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       8 FSASW 12


Search completed: January 29, 2003, 14:12:57
Job time : 16 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:15:53 ; Search time 15 Seconds
(without alignments)
32.045 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	9	2	A24244	adipokinetic hormo
2	16	80.0	8	2	A28004	adipokinetic hormo
3	16	80.0	10	2	A31571	hypertrehalosemic/
4	15	75.0	8	2	S10596	adipokinetic hormo
5	15	75.0	9	2	D57444	neuropeptide Grb-A
6	15	75.0	10	2	T17063	cytochrome-c oxida
7	15	75.0	10	2	T12325	cytochrome-c oxida
8	15	75.0	10	2	S53789	neuropeptide Pec-H
9	15	75.0	15	2	PH1613	Ig H chain V-D-J r
10	15	75.0	17	2	A34704	protein-tyrosine k
11	15	75.0	20	2	S77981	cytochrome-c oxida
12	15	75.0	20	2	PN0171	peptidylprolyl iso
13	15	75.0	20	2	PH1380	alpha-amylase (EC
14	14	70.0	8	2	A61348	red pigment-concen
15	14	70.0	8	2	S08995	hypertrehalosemic
16	14	70.0	8	2	S08996	hypertrehalosemic
17	14	70.0	8	2	A49823	adipokinetic hormo
18	14	70.0	8	2	B49823	adipokinetic hormo
19	14	70.0	8	2	A44960	neuropeptide Led-C
20	14	70.0	8	2	B44960	neuropeptide Led-C
21	14	70.0	8	2	A43976	hypertrehalosemic
22	14	70.0	8	2	B43976	hypertrehalosemic
23	14	70.0	8	2	A33995	adipokinetic hormo
24	14	70.0	8	2	S11545	adipokinetic hormo
25	14	70.0	8	2	S55310	adipokinetic hormo
26	14	70.0	8	2	A58620	adipokinetic hormo
27	14	70.0	8	2	A05169	neuropeptide M-I -
28	14	70.0	10	2	A60421	hypertrehalosemic
29	14	70.0	10	2	S08997	hypertrehalosemic
30	14	70.0	10	2	S08998	hypertrehalosemic
31	14	70.0	10	2	A26381	hypertrehalosemic
32	14	70.0	10	2	JC1416	hypertrehalosemic
33	14	70.0	10	2	S09138	hypertrehalosemic
34	14	70.0	10	2	B33995	hypotrehalosemic h
35	14	70.0	10	2	C39191	hypothetical prote
36	14	70.0	10	2	PT0322	Ig heavy chain CRD
37	14	70.0	10	2	T17066	cytochrome-c oxida
38	14	70.0	10	2	T17069	cytochrome-c oxida
39	14	70.0	10	2	T12329	cytochrome-c oxida
40	14	70.0	12	2	PT0274	Ig heavy chain CRD
41	14	70.0	12	2	PH1324	Ig heavy chain DJ
42	14	70.0	13	2	PC4391	cysteine proteinas
43	14	70.0	16	2	C37290	homeotic protein G
44	14	70.0	19	2	S32675	nitrogen fixation
45	14	70.0	20	2	PC1240	calcium-binding pr

ALIGNMENTS

RESULT 1
A24244
adipokinetic hormone - bollworm
N;Alternate names: Hez-AKH
C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C;Date: 31-Mar-1988 #sequenc... ...sion 23-Mar-1995 #text_change 31-Oct-1997
C;Accession: ...
...T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridg
..., 622-628, 1986
...icture of a peptide from the corpora cardiaca of He
...186794; PMID:3964263
A
C
C ...corpora cardiaca; hormone; neuropeptide; pyrogluta
F; ...xylic acid (Gln) #status experimental
F; ...end (Gly) #status experimental

Seq length ≤ 20

...ore 17; DB 2; Length 9;
...ted. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FTSSW 8

RESULT 2
A28004
adipokinetic hormone G - two-spotted cricket
N;Alternate names: AKH-G
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997
C;Accession: A28004
R;Gaede, G.; Rinehart, K.L.
Biochem. Biophys. Res. Commun. 149, 908-914, 1987
A;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a pe
A;Reference number: A28004; MUID:88106553; PMID:3426616
A;Accession: A28004
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we h
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 80.0%; Score 16; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 FXXXW 5
           |   |
Db       4 FSTGW 8


RESULT 3
A31571
hypertrehalosemic/adipokinetic hormone - bollworm
N;Alternate names: Hez-HrTH
C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C;Date: 30-Jun-1989 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C;Accession: A31571
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S
Biochem. Biophys. Res. Commun. 155, 344-350, 1988
A;Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea wi
A;Reference number: A31571; MUID:88326324; PMID:3415690
A;Accession: A31571
A;Molecule type: protein
A;Residues: 1-10 <JAF>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Asn) #status experimental

  Query Match             80.0%;  Score 16;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 6.5e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSSGW 8


RESULT 4
S10596
adipokinetic hormone - pond skimmer
C;Species: Libellula auripennis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997
C;Accession: S10596
R;Gaede, G.
Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating ho
A;Reference number: S10596; MUID:90359055; PMID:2390213
A;Accession: S10596
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Comment: This peptide has both adipokinetic and hypertrehalosemic activities.
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

  Query Match             75.0%;  Score 15;  DB 2;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FTPSW 8


RESULT 5
D57444
neuropeptide Grb-AST B4 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: D57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: D57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

  Query Match             75.0%;  Score 15;  DB 2;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       5 FHGSW 9


RESULT 6
T17063
cytochrome-c oxidase (EC 1.9.3.1) chain I - Hoplocercus spinosus mitochondrion (fragm
C;Species: mitochondrion Hoplocercus spinosus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C;Accession: T17063
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial
A;Reference number: Z18674; MUID:97315309; PMID:9169559
A;Accession: T17063
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U82683; NID:g3603124; PID:g3603127; PIDN:AAC62284.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

  Query Match             75.0%;  Score 15;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       2 FISRW 6


RESULT 7
T12325
cytochrome-c oxidase (EC 1.9.3.1) chain I - Leiocephalus carinatus mitochondrion (fra
C;Species: mitochondrion Leiocephalus carinatus
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999
C;Accession: T12325
R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example
A;Reference number: Z17488; MUID:99162288; PMID:10051389
A;Accession: T12325
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <SCH>
A;Cross-references: EMBL:AF049864; NID:g4105754; PID:g4105757; PIDN:AAD02535.1
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

  Query Match             75.0%;  Score 15;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       2 FITRW 6


RESULT 8
S53789
neuropeptide Pec-HrTH - Platypleura capensis
```

C;Species: Platypleura capensis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S53789
R;Gaede, G.; Janssens, M.P.E.
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
A;Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalc
A;Reference number: S53789; MUID:95225985; PMID:7710694
A;Accession: S53789
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Keywords: blocked amino end; blocked carboxyl end

Query Match 75.0%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FSPSW 8

RESULT 9
PH1613
Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1613
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1613
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 75.0%; Score 15; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 10 FTMLW 14

RESULT 10
A34704
protein-tyrosine kinase (EC 2.7.1.112) 1, neuron-specific - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 04-Feb-2000
C;Accession: A34704
R;Pyper, J.M.; Bolen, J.B.
Mol. Cell. Biol. 10, 2035-2040, 1990
A;Title: Identification of a novel neuronal C-SRC exon expressed in human brain.
A;Reference number: A34704; MUID:90220588; PMID:1691439
A;Accession: A34704
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-17 <PYP>
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 75.0%; Score 15; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 10 FTFRW 14

RESULT 11
S77981
cytochrome-c oxidase (EC 1.9.3.1) chain Va.1 - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 26-Feb-1998
C;Accession: S77981
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A;Reference number: S77980
A;Accession: S77981
A;Molecule type: protein
A;Residues: 1-20 <ARN>
A;Experimental source: heart; liver
C;Genetics:
A;Genome: nuclear
C;Function:
A;Pathway: oxidative phosphorylation; respiratory chain
C;Superfamily: mammalian cytochrome-c oxidase chain Va
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membr

Query Match 75.0%; Score 15; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 11 FDARW 15

RESULT 12
PN0171
peptidylprolyl isomerase (EC 5.2.1.8) b, cytosolic - fungus (Fusarium sporotrichioide
N;Contains: cyclophilin
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 02-Sep-2000
C;Accession: PN0171
R;Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr
A;Reference number: PN0160
A;Accession: PN0171
A;Molecule type: protein
A;Residues: 1-20 <FUK>
A;Experimental source: strain M-1-1
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclosporin A binding; cytosol

Query Match 75.0%; Score 15; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 6 FDITW 10

RESULT 13
PH1380
alpha-amylase (EC 3.2.1.1) (Haim sensitive) - Bacillus sp. (fragment)
C;Species: Bacillus sp.
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 07-May-1999
C;Accession: PH1380
R;Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.
Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992
A;Title: Purification and some properties of a Haim-sensitive alpha-amylase from newl
A;Reference number: PH1380; MUID:93113087; PMID:1369074
A;Accession: PH1380
A;Molecule type: protein
A;Residues: 1-20 <KAW>
A;Experimental source: strain N0.195
C;Comment: This enzyme has an optimum pH of 7.0.
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 75.0%; Score 15; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 FXXXW 5
           |   |
Db      13 FSWTW 17
```

RESULT 14
A61348
red pigment-concentrating hormone - northern shrimp
N;Alternate names: blanching hormone
C;Species: Pandalus borealis (northern shrimp)
C;Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C;Accession: A61348; S07139
R;Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A;Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A;Reference number: A61348; MUID:72228738; PMID:5041363
A;Accession: A61348
A;Molecule type: protein
A;Residues: 1-8 <FER1>
R;Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A;Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus bore
A;Reference number: S07139; MUID:75054965; PMID:4433569
A;Accession: S07139
A;Molecule type: protein
A;Residues: 'E',2-8 <FER2>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi
zed pigment-containing cells.
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutami
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 70.0%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 FXXXW 5
           |   |
Db       4 FSPGW 8
```

RESULT 15
S08995
hypertrehalosemic hormone I - oriental cockroach
N;Alternate names: Pea-CAH-I
C;Species: Blatta orientalis (oriental cockroach)
C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Accession: S08995
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpor
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08995
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 70.0%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 FXXXW 5
           |   |
Db       4 FSPNW 8
```

Search completed: January 29, 2003, 14:17:59
Job time : 15 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:13:03 ; Search time 10 Seconds
(without alignments)
20.738 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1147

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	80.0	8	1	AKHG_GRYBI	P14086 gryllus bim
2	16	80.0	10	1	HTF_HELZE	P16353 heliothis z
3	15	75.0	8	1	AKH_LIBAU	P25418 libellula a
4	15	75.0	10	1	AKHX_LOCMI	P81626 locusta mig
5	15	75.0	20	1	COXA_THUOB	P80972 thunnus obe
6	14	70.0	8	1	AKH_TABAT	P14595 tabanus atr
7	14	70.0	8	1	HTF1_PERAM	P04548 periplaneta
8	14	70.0	8	1	HTF2_PERAM	P04549 periplaneta
9	14	70.0	8	1	HTF_TENMO	P25419 tenebrio mo
10	14	70.0	8	1	RPCH_PANBO	P08939 pandalus bo
11	14	70.0	10	1	HTF1_ROMMI	P18110 romalea mic
12	14	70.0	10	1	HTF2_CARMO	P11385 carausius m
13	14	70.0	10	1	HTF_NAUCI	P10939 nauphoeta c
14	14	70.0	10	1	HTF_TABAT	P14596 tabanus atr
15	14	70.0	13	1	YPNP_PHOLU	P41122 photorhabdu
16	14	70.0	20	1	CRTC_SPIOL	P30806 spinacia ol
17	13	65.0	6	1	EI01_LITRU	P82096 litoria rub
18	12	60.0	10	1	GON1_PETMA	P04378 petromyzon
19	12	60.0	11	1	CA31_LITCI	P82089 litoria cit
20	12	60.0	11	1	CA32_LITCI	P82090 litoria cit
21	12	60.0	11	1	CORZ_PERAM	P11496 periplaneta
22	11	55.0	4	1	OCP3_OCTMI	P58649 octopus min
23	11	55.0	5	1	BPP7_BOTIN	P30425 bothrops in
24	11	55.0	5	1	UF01_MOUSE	P38639 mus musculu
25	11	55.0	6	1	LOK1_LOCMI	P41491 locusta mig
26	11	55.0	7	1	BRHP_CONIM	P58803 conus imper
27	11	55.0	7	1	TY51_LITRU	P82065 litoria rub
28	11	55.0	7	1	WWA1_ACHFU	P35919 achatina fu
29	11	55.0	7	1	WWA2_ACHFU	P35920 achatina fu
30	11	55.0	7	1	WWA3_ACHFU	P35921 achatina fu
31	11	55.0	8	1	ACI_THUAL	P18691 thunnus alb
32	11	55.0	8	1	AKH_MELML	P25423 melolontha
33	11	55.0	8	1	CCKN_MACEU	P30369 macropus eu
34	11	55.0	8	1	COW2_CONPU	P58785 conus purpu
35	11	55.0	8	1	LCK1_LEUMA	P21140 leucophaea
36	11	55.0	8	1	LCK2_LEUMA	P21141 leucophaea
37	11	55.0	8	1	LCK3_LEUMA	P21142 leucophaea
38	11	55.0	8	1	LCK4_LEUMA	P21143 leucophaea
39	11	55.0	8	1	LCK5_LEUMA	P19987 leucophaea
40	11	55.0	8	1	LCK6_LEUMA	P19988 leucophaea
41	11	55.0	8	1	LCK7_LEUMA	P19989 leucophaea
42	11	55.0	8	1	LCK8_LEUMA	P19990 leucophaea
43	11	55.0	8	1	PLP_BRANA	P81707 brassica na
44	11	55.0	9	1	COW_CONVE	P83047 conus ventr
45	11	55.0	9	1	D1_NEPNO	P24816 nephrops no

ALIGNMENTS

RESULT 1
AKHG_GRYBI
ID AKHG_GRYBI STANDARD; PRT; 8 AA.
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;
OC Gryllidae; Gryllinae; Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokinetic activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A28004; A28004.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 80.0%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1 FXXXW 5
           | |
Db       4 FSTGW 8
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RESULT 2
HTF_HELZE
ID HTF_HELZE STANDARD; PRT; 10 AA.

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AC   P16353;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Hypertrehalosaemic hormone (Hez-HRTH).
OS   Heliothis zea (Corn earworm) (Bollworm).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC   Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.
OX   NCBI_TaxID=7113;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=88326324; PubMed=3415690;
RA   Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
RA   Tseng C.M., Zhang Y.S., Hayes D.K.;
RT   "Isolation and primary structure of a neuropeptide hormone from
RT   Heliothis zea with hypertrehalosemic and adipokinetic activities.";
RL   Biochem. Biophys. Res. Commun. 155:344-350(1988).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A31571; A31571.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1096 MW;  8E70367865A5B9D1 CRC64;

  Query Match             80.0%;  Score 16;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSSGW 8


RESULT 3
AKH_LIBAU
ID   AKH_LIBAU      STANDARD;      PRT;     8 AA.
AC   P25418;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Adipokinetic hormone (AKH).
OS   Libellula auripennis (Skimmer dragonfly).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae;
OC   Libellula.
OX   NCBI_TaxID=6966;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90359055; PubMed=2390213;
RA   Gaede G.;
RT   "The putative ancestral peptide of the adipokinetic/red-pigment-
RT   concentrating hormone family isolated and sequenced from a
RT   dragonfly.";
RL   Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC   -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC       CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC       DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC       MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; S10596; S10596.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  978 MW;  8665A771A9C452D6 CRC64;

  Query Match             75.0%;  Score 15;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FTPSW 8


RESULT 4
AKHX_LOCMI
ID   AKHX_LOCMI      STANDARD;      PRT;     10 AA.
AC   P81626;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Peptide hormone.
OS   Locusta migratoria (Migratory locust).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC   Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
OX   NCBI_TaxID=7004;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RA   Siegert K.J.;
RL   Submitted (DEC-1998) to the SWISS-PROT data bank.
CC   -!- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LOCUST
CC       INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.
CC   -!- SIMILARITY: SOME SIMILARITY TO THE AKH / HRTH / RPCH FAMILY.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1222 MW;  81BFF67AB415B9D1 CRC64;

  Query Match             75.0%;  Score 15;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 5.1e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSRDW 8


RESULT 5
COXA_THUOB
ID   COXA_THUOB      STANDARD;      PRT;     20 AA.
AC   P80972;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cytochrome c oxidase polypeptide Va-1 (EC 1.9.3.1) (Fragment).
OS   Thunnus obesus (Bigeye tuna).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC   Scombridae; Thunnus.
OX   NCBI_TaxID=8241;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart, and Liver;
RX   MEDLINE=97454291; PubMed=9310366;
RA   Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA   Kadenbach B.;
RT   "The subunit structure of cytochrome-c oxidase from tuna heart and
RT   liver.";
RL   Eur. J. Biochem. 248:99-103(1997).
CC   -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC       OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
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CC   -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC       c + 2 H(2)O.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR   InterPro; IPR003204; Cyt_c_ox5A.
DR   Pfam; PF02284; COX5A; 1.
KW   Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2404 MW;  7E82E43B7157355E CRC64;

  Query Match             75.0%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 8.6e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      11 FDARW 15


RESULT 6
AKH_TABAT
ID   AKH_TABAT      STANDARD;      PRT;     8 AA.
AC   P14595;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE   (DCC I).
OS   Tabanus atratus (Horse fly).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC   Tabanomorpha; Tabanidae; Tabanus.
OX   NCBI_TaxID=7207;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90046758; PubMed=2813385;
RA   Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA   Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT   "Primary structure of two neuropeptide hormones with adipokinetic and
RT   hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT   flies (Diptera).";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC   -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC       CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC       DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC       MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A33995; A33995.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  949 MW;  86786771A9D1A736 CRC64;

  Query Match             70.0%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FTPGW 8


RESULT 7
HTF1_PERAM
ID   HTF1_PERAM     STANDARD;      PRT;     8 AA.
AC   P04548;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
DE   (PeA-CAH-I) (LeD-CC-I) (Hypertrehalosaemic neuropeptide I).
OS   Periplaneta americana (American cockroach),
OS   Leptinotarsa decemlineata (Colorado potato beetle), and
OS   Blatta orientalis (Oriental cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blattoidea; Blattidae; Periplaneta.
OX   NCBI_TaxID=6978, 7539, 6976;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=P.americana;
RX   MEDLINE=85046530; PubMed=6548628;
RA   Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA   Rinehart K.L. Jr.;
RT   "Structures of two cockroach neuropeptides assigned by fast atom
RT   bombardment mass spectrometry.";
RL   Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=P.americana;
RX   MEDLINE=84298179; PubMed=6591205;
RA   Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA   Miller C.A., Schooley D.A.;
RT   "Isolation and primary structure of two peptides with
RT   cardioacceleratory and hyperglycemic activity from the corpora
RT   cardiaca of Periplaneta americana.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX   MEDLINE=90160053; PubMed=2576128;
RA   Gaede G., Kellner R.;
RT   "The metabolic neuropeptides of the corpus cardiacum from the potato
RT   beetle and the American cockroach are identical.";
RL   Peptides 10:1287-1289(1989).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX   MEDLINE=90253659; PubMed=2340112;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT   the corpora cardiaca of the cockroaches Leucophaea maderae,
RT   Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT   and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT   atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A05169; A05169.
DR   PIR; S08995; S08995.
DR   PIR; A49823; A49823.
DR   PIR; A44960; A44960.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  991 MW;  86745775B9C452D6 CRC64;

  Query Match             70.0%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSPNW 8


RESULT 8
HTF2_PERAM
ID   HTF2_PERAM     STANDARD;      PRT;     8 AA.
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AC   P04549;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
DE   (PeA-CAH-II) (LeD-CC-II) (Hypertrehalosaemic neuropeptide II).
OS   Periplaneta americana (American cockroach),
OS   Leptinotarsa decemlineata (Colorado potato beetle), and
OS   Blatta orientalis (Oriental cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blattoidea; Blattidae; Periplaneta.
OX   NCBI_TaxID=6978, 7539, 6976;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=P.americana;
RX   MEDLINE=85046530; PubMed=6548628;
RA   Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA   Rinehart K.L. Jr.;
RT   "Structures of two cockroach neuropeptides assigned by fast atom
RT   bombardment mass spectrometry.";
RL   Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=P.americana;
RX   MEDLINE=84298179; PubMed=6591205;
RA   Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA   Miller C.A., Schooley D.A.;
RT   "Isolation and primary structure of two peptides with
RT   cardioacceleratory and hyperglycemic activity from the corpora
RT   cardiaca of Periplaneta americana.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX   MEDLINE=90160053; PubMed=2576128;
RA   Gaede G., Kellner R.;
RT   "The metabolic neuropeptides of the corpus cardiacum from the potato
RT   beetle and the American cockroach are identical.";
RL   Peptides 10:1287-1289(1989).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX   MEDLINE=90253659; PubMed=2340112;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT   the corpora cardiaca of the cockroaches Leucophaea maderae,
RT   Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT   and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT   atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A05170; A05170.
DR   PIR; S08996; S08996.
DR   PIR; B44960; B44960.
DR   PIR; B49823; B49823.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  1006 MW;  86745771A9D1A736 CRC64;

  Query Match             70.0%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
            |   |
Db       4 FTPNW 8
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RESULT 9
HTF_TENMO
ID   HTF_TENMO      STANDARD;      PRT;     8 AA.
AC   P25419;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Hypertrehalosaemic factor (HOTH) (Hypertrehalosemic neuropeptide).
OS   Tenebrio molitor (Yellow mealworm), and
OS   Zophobas rugipes.
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC   Cucujiformia; Tenebrionidae; Tenebrio.
OX   NCBI_TaxID=7067, 7075;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90341081; PubMed=2381871;
RA   Gaede G., Rosinski G.;
RT   "The primary structure of the hypertrehalosemic neuropeptide from
RT   tenebrionid beetles: a novel member of the AKH/RPCH family.";
RL   Peptides 11:455-459(1990).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A43976; A43976.
DR   PIR; B43976; B43976.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  1005 MW;  86745775B9C44736 CRC64;

  Query Match             70.0%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
            |   |
Db       4 FSPNW 8


RESULT 10
RPCH_PANBO
ID   RPCH_PANBO     STANDARD;      PRT;     8 AA.
AC   P08939;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Red pigment concentrating hormone (RPCH).
OS   Pandalus borealis (Northern red shrimp).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC   Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC   Caridea; Pandaloidea; Pandalidae; Pandalus.
OX   NCBI_TaxID=6703;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75054965; PubMed=4433569;
RA   Fernlund P.;
RT   "Structure of the red-pigment-concentrating hormone of the shrimp,
RT   Pandalus borealis.";
RL   Biochim. Biophys. Acta 371:304-311(1974).
CC   -!- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY
CC       STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-
CC       CHROMATOPHORES.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; S07139; S07139.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
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KW   Pigment; Hormone; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  948 MW;  86786775B9C44736 CRC64;

  Query Match             70.0%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSPGW 8


RESULT 11
HTF1_ROMMI
ID   HTF1_ROMMI     STANDARD;      PRT;    10 AA.
AC   P18110;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   RO I (Hypertrehalosaemic factor).
OS   Romalea microptera (Lubber grasshopper).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC   Acridomorpha; Acridoidea; Romaleidae; Romalea.
OX   NCBI_TaxID=7007;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=89145002; PubMed=3226948;
RA   Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT   "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT   the lubber grasshopper, Romalea microptera.";
RL   Peptides 9:681-688(1988).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1163 MW;  056236745771A9C4 CRC64;

  Query Match             70.0%;  Score 14;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 8.8e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FTPNW 8


RESULT 12
HTF2_CARMO
ID   HTF2_CARMO     STANDARD;      PRT;    10 AA.
AC   P11385;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic
DE   neuropeptide II).
OS   Carausius morosus (Indian stick insect), and
OS   Extatosoma tiaratum (Stick insect).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Orthopteroidea; Phasmatodea;
OC   Heteronemiidae; Carausius.
OX   NCBI_TaxID=7022, 7024;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX   MEDLINE=87157103; PubMed=3828078;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structure of the hypertrehalosaemic factor II from the
RT   corpus cardiacum of the Indian stick insect, Carausius morosus,
RT   determined by fast atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
RX   MEDLINE=90253659; PubMed=2340112;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT   the corpora cardiaca of the cockroaches Leucophaea maderae,
RT   Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT   and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT   atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN   [3]
RP   CARBOHYDRATE-LINKAGE SITE.
RC   SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX   MEDLINE=93129188; PubMed=1482345;
RA   Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT   "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT   a stick insect corpus cardiacum.";
RL   Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; S07157; S07157.
DR   PIR; S09138; S09138.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Glycoprotein.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   CARBOHYD      8      8       C-LINKED (MAN) (PROBABLE).
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1164 MW;  9B9036745771A9D1 CRC64;

  Query Match             70.0%;  Score 14;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 8.8e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FTPNW 8


RESULT 13
HTF_NAUCI
ID   HTF_NAUCI      STANDARD;      PRT;    10 AA.
AC   P10939;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypertrehalosaemic hormone (HTH) (Hypertrehalosaemic neuropeptide).
OS   Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS   Leucophaea maderae (Madeira cockroach),
OS   Blattella germanica (German cockroach), and
OS   Gromphadorina portentosa (Madagascan hissing cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blaberoidea; Blaberidae; Nauphoeta.
OX   NCBI_TaxID=6990, 6988, 6973, 36953;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=N.cinerea; TISSUE=Corpora cardiaca;
RX   MEDLINE=87100208; PubMed=3801028;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Amino acid sequence of a hypertrehalosaemic neuropeptide from the
RT   corpus cardiacum of the cockroach, Nauphoeta cinerea.";
RL   Biochem. Biophys. Res. Commun. 141:774-781(1986).
```

```
RN   [2]
RP   SEQUENCE.
RC   SPECIES=L.maderae, G.portentosa, and B.germanica;
RX   MEDLINE=90253659; PubMed=2340112;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT   the corpora cardiaca of the cockroaches Leucophaea maderae,
RT   Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT   and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT   atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=B.germanica;
RX   MEDLINE=91179584; PubMed=2080017;
RA   Veenstra J.A., Camps F.;
RT   "Structure of the hypertrehalosemic neuropeptide of the German
RT   cockroach, Blattella germanica.";
RL   Neuropeptides 15:107-109(1990).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; A26381; A26381.
DR   PIR; S08997; S08997.
DR   PIR; S08998; S08998.
DR   PIR; S09137; S09137.
DR   PIR; A60421; A60421.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1092 MW;  056236786775B9C4 CRC64;

  Query Match             70.0%;  Score 14;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 8.8e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSPGW 8


RESULT 14
HTF_TABAT
ID   HTF_TABAT      STANDARD;      PRT;    10 AA.
AC   P14596;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
DE   (DCC II).
OS   Tabanus atratus (Horse fly).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC   Tabanomorpha; Tabanidae; Tabanus.
OX   NCBI_TaxID=7207;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90046758; PubMed=2813385;
RA   Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA   Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT   "Primary structure of two neuropeptide hormones with adipokinetic and
RT   hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT   flies (Diptera).";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC   -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC       ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC       THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; B33995; B33995.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1169 MW;  916036786771A9D1 CRC64;

  Query Match             70.0%;  Score 14;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 8.8e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FTPGW 8


RESULT 15
YPNP_PHOLU
ID   YPNP_PHOLU     STANDARD;      PRT;    13 AA.
AC   P41122;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein in PNP 3'region (ORF3) (Fragment).
OS   Photorhabdus luminescens (Xenorhabdus luminescens).
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Photorhabdus.
OX   NCBI_TaxID=29488;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K122;
RX   MEDLINE=94266731; PubMed=8206856;
RA   Clarke D.J., Dowds B.C.A.;
RT   "The gene coding for polynucleotide phosphorylase in Photorhabdus sp.
RT   strain K122 is induced at low temperatures.";
RL   J. Bacteriol. 176:3775-3784(1994).
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X76069; CAA53672.1; -.
KW   Hypothetical protein.
FT   NON_TER       13     13
SQ   SEQUENCE   13 AA;  1634 MW;  64774A4F6267A364 CRC64;

  Query Match             70.0%;  Score 14;  DB 1;  Length 13;
  Best Local Similarity   40.0%;  Pred. No. 1.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       3 FFLRW 7


Search completed: January 29, 2003, 14:17:03
Job time : 10 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:15:28 ; Search time 28 Seconds
(without alignments)
36.794 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 6395

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	13	8	Q9XLI2	Q9xli2 bemisia tab
2	16	80.0	11	8	Q9G649	Q9g649 otocryptis
3	16	80.0	17	4	O15276	O15276 homo sapien
4	16	80.0	19	15	O91329	O91329 human immun
5	16	80.0	19	15	Q9WJB1	Q9wjb1 human immun
6	15	75.0	9	8	Q8WGE6	Q8wge6 procambarus
7	15	75.0	10	8	Q9ZYT2	Q9zyt2 leiocephalu
8	15	75.0	10	8	P92707	P92707 platysaurus
9	15	75.0	10	8	O79897	O79897 hoplocercus
10	15	75.0	11	8	Q9G368	Q9g368 draco blanf
11	15	75.0	11	8	Q9G646	Q9g646 sitana pont
12	15	75.0	11	8	Q9G643	Q9g643 calotes cal
13	15	75.0	11	8	Q9G640	Q9g640 calotes cey
14	15	75.0	11	8	Q9G634	Q9g634 calotes lio
15	15	75.0	11	8	Q9G631	Q9g631 calotes nig
16	15	75.0	11	8	Q9G365	Q9g365 calotes emm
17	15	75.0	11	8	Q9G628	Q9g628 calotes mys
18	15	75.0	11	8	Q9G625	Q9g625 calotes ver
19	15	75.0	11	8	Q9G601	Q9g601 bronchocela
20	15	75.0	11	8	Q9G5Z2	Q9g5z2 pseudocalot
21	15	75.0	11	8	Q9G5Y9	Q9g5y9 pseudocalot
22	15	75.0	11	8	Q8WES0	Q8wes0 ceratophora
23	15	75.0	20	2	Q9R5E8	Q9r5e8 bacillus sp
24	15	75.0	20	6	Q95MK5	Q95mk5 varecia var
25	14	70.0	10	8	Q9ZYS6	Q9zys6 stenocercus
26	14	70.0	10	8	O79885	O79885 anolis pate
27	14	70.0	10	8	O79903	O79903 oplurus cuv
28	14	70.0	10	8	O79906	O79906 phrynosoma
29	14	70.0	10	8	Q9T8X1	Q9t8x1 liolaemus a
30	14	70.0	10	8	Q9T8U8	Q9t8u8 liolaemus p
31	14	70.0	10	8	Q8WDI8	Q8wdi8 anolis tran
32	14	70.0	10	8	Q8WDH8	Q8wdh8 anolis mest
33	14	70.0	10	8	Q8WDH6	Q8wdh6 anolis wood
34	14	70.0	10	8	Q8WDH4	Q8wdh4 anolis carp
35	14	70.0	10	8	Q8WDH2	Q8wdh2 anolis lemu
36	14	70.0	10	8	Q8WDH0	Q8wdh0 anolis limi
37	14	70.0	10	8	Q8WDG6	Q8wdg6 anolis trac
38	14	70.0	10	8	Q8W971	Q8w971 anolis fusc
39	14	70.0	10	8	Q8W970	Q8w970 anolis nite
40	14	70.0	10	8	Q8W969	Q8w969 anolis orto
41	14	70.0	10	8	Q8W8Q4	Q8w8q4 anolis punc
42	14	70.0	10	8	Q8W8Q3	Q8w8q3 anolis nite
43	14	70.0	10	8	Q8W8Q2	Q8w8q2 anolis punc
44	14	70.0	10	8	Q8W7U4	Q8w7u4 anolis nite
45	14	70.0	12	2	Q53579	Q53579 rhodobacter

ALIGNMENTS

RESULT 1
Q9XLI2
ID Q9XLI2 PRELIMINARY; PRT; 13 AA.
AC Q9XLI2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome oxidase I (Fragment).
OS Bemisia tabaci (Sweetpotato whitefly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
OC Aleyrodiformes; Aleyrodoidea; Aleyrodidae; Aleyrodinae; Bemisia.
OX NCBI_TaxID=7038;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10583831;
RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,
RA Brown J.K.;
RT "A phylogeographical analysis of the Bemisia tabaci species complex
RT based on mitochondrial DNA markers.";
RL Mol. Ecol. 8:1683-1691(1999).
DR EMBL; AF110703; AAD28415.1; -.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;

Query Match 85.0%; Score 17; DB 8; Length 13;
Best Local Similarity 40.0%; Pred. No. 8.2e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 FXXXW 5
          |   |
Db      3 FTSSW 7
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RESULT 2
Q9G649
ID Q9G649 PRELIMINARY; PRT; 11 AA.

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AC   Q9G649;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Otocryptis wiegmanni.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC   Otocryptis.
OX   NCBI_TaxID=118220;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A.;
RT   "Evolution and information content of the mitochondrial genomic
RT   structural features illustrated with acrodont lizards.";
RL   Syst. Biol. 49:257-277(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA   Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT   "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT   phylogenetics.";
RL   Syst. Biol. 49:233-256(2000).
DR   EMBL; AF128480; AAG00677.1; -.
KW   Mitochondrion.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1347 MW;  932D3710D3640DC1 CRC64;

  Query Match             80.0%;  Score 16;  DB 8;  Length 11;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       3 FTARW 7


RESULT 3
O15276
ID   O15276      PRELIMINARY;      PRT;    17 AA.
AC   O15276;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Mitochondrial translation elongation factor EF-Tu (Fragment).
GN   TUFM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jacobs H.T., Smurthwaite L., Koshy R.;
RT   "Human genomic sequences encoding mitochondrial elongation factor EF-
RT   Tu: Evidence for post-endosymbiotic intron insertion.";
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y11797; CAA72493.1; -.
KW   Elongation factor.
FT   NON_TER      1      1
FT   NON_TER     17     17
SQ   SEQUENCE   17 AA;  2019 MW;  BF737D12D2AB0A7E CRC64;

  Query Match             80.0%;  Score 16;  DB 4;  Length 17;
  Best Local Similarity   40.0%;  Pred. No. 1.8e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FSLTW 5


RESULT 4
O91329
ID   O91329      PRELIMINARY;      PRT;    19 AA.
AC   O91329;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope glycoprotein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98285741; PubMed=9621043;
RA   Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,
RA   Safar M., Barre-Sinoussi F., Kazatchkine M.D.;
RT   "Genetically related human immunodeficiency virus type 1 in three
RT   adults of a family with no identified risk factor for intrafamilial
RT   transmission.";
RL   J. Virol. 72:5831-5839(1998).
DR   EMBL; U87220; AAC32980.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER      1      1
SQ   SEQUENCE   19 AA;  2324 MW;  379CB14A9E073911 CRC64;

  Query Match             80.0%;  Score 16;  DB 15;  Length 19;
  Best Local Similarity   40.0%;  Pred. No. 2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      10 FNSTW 14


RESULT 5
Q9WJB1
ID   Q9WJB1      PRELIMINARY;      PRT;    19 AA.
AC   Q9WJB1;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Envelope glycoprotein (Fragment).
GN   ENV.
OS   Human immunodeficiency virus type 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98285741; PubMed=9621043;
RA   Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,
RA   Safar M., Barre-Sinoussi F., Kazatchkine M.D.;
RT   "Genetically related human immunodeficiency virus type 1 in three
RT   adults of a family with no identified risk factor for intrafamilial
RT   transmission.";
RL   J. Virol. 72:5831-5839(1998).
DR   EMBL; U87216; AAC32976.1; -.
KW   AIDS; Coat protein; Glycoprotein.
FT   NON_TER      1      1
SQ   SEQUENCE   19 AA;  2294 MW;  3781714A9E073911 CRC64;

  Query Match             80.0%;  Score 16;  DB 15;  Length 19;
  Best Local Similarity   40.0%;  Pred. No. 2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      10 FNSTW 14


RESULT 6
Q8WGE6
ID   Q8WGE6      PRELIMINARY;      PRT;     9 AA.
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AC   Q8WGE6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Cytochrome oxidase subunit 1 (Fragment).
OS   Procambarus clarkii (Red swamp crayfish).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC   Astacoidea; Cambaridae; Procambarus.
OX   NCBI_TaxID=6728;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
RA   Cunningham C.W.;
RT   "Mitochondrial gene rearrangements support a hypothesis of parallel
RT   evolution to the crab-like form.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF436024; AAL31599.1; -.
KW   Mitochondrion.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1185 MW;  936BB9C733640321 CRC64;

  Query Match             75.0%;  Score 15;  DB 8;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 6.7e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      1 FTKRW 5


RESULT 7
Q9ZYT2
ID   Q9ZYT2      PRELIMINARY;      PRT;    10 AA.
AC   Q9ZYT2;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Leiocephalus carinatus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae;
OC   Leiocephalus.
OX   NCBI_TaxID=81825;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99162288; PubMed=10051389;
RA   Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT   "Molecular tests of phylogenetic taxonomies: A general procedure and
RT   example using four subfamilies of the lizard family Iguanidae.";
RL   Mol. Phylogenet. Evol. 10:367-376(1998).
DR   EMBL; AF049864; AAD02535.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1302 MW;  0A3480C7336411A0 CRC64;

  Query Match             75.0%;  Score 15;  DB 8;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      2 FITRW 6


RESULT 8
P92707
ID   P92707      PRELIMINARY;      PRT;    10 AA.
AC   P92707;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Platysaurus capensis.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
OC   Cordylidae; Platysaurus.
OX   NCBI_TaxID=52175;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97153826; PubMed=9000757;
RA   Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
RT   "Two novel gene orders and the role of light-strand replication in
RT   rearrangement of the vertebrate mitochondrial genome.";
RL   Mol. Biol. Evol. 14:91-104(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97153820; PubMed=9000751;
RA   Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT   "Replication slippage may cause parallel evolution in the secondary
RT   structures of mitochondrial transfer RNAs.";
RL   Mol. Biol. Evol. 14:30-39(1997).
DR   EMBL; U71329; AAB48286.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1322 MW;  0A3480C9D36415B0 CRC64;

  Query Match             75.0%;  Score 15;  DB 8;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      2 FISRW 6


RESULT 9
O79897
ID   O79897      PRELIMINARY;      PRT;    10 AA.
AC   O79897;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Hoplocercus spinosus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;
OC   Hoplocercus.
OX   NCBI_TaxID=52193;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97315309; PubMed=9169559;
RA   Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT   "Evolutionary shifts in three major structural features of the
RT   mitochondrial genome among iguanian lizards.";
RL   J. Mol. Evol. 44:660-674(1997).
DR   EMBL; U82683; AAC62284.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1288 MW;  0A3480C7336415B0 CRC64;

  Query Match             75.0%;  Score 15;  DB 8;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      2 FISRW 6
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RESULT 10
Q9G368
ID   Q9G368       PRELIMINARY;      PRT;    11 AA.
AC   Q9G368;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Draco blanfordii.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC   Draco.
OX   NCBI_TaxID=89021;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97153820; PubMed=9000751;
RA   Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT   "Replication slippage may cause parallel evolution in the secondary
RT   structures of mitochondrial transfer RNAs.";
RL   Mol. Biol. Evol. 14:30-39(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A.;
RT   "Evolution and information content of the mitochondrial genomic
RT   structural features illustrated with acrodont lizards.";
RL   Syst. Biol. 49:257-277(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA   Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT   "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT   phylogenetics.";
RL   Syst. Biol. 49:233-256(2000).
DR   EMBL; AF128477; AAG00668.1; -.
KW   Mitochondrion.
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SQ   SEQUENCE   11 AA;  1341 MW;  4B2D371E336415B7 CRC64;

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Qy       1 FXXXW 5
           |   |
Db       3 FLSRW 7


RESULT 11
Q9G646
ID   Q9G646       PRELIMINARY;      PRT;    11 AA.
AC   Q9G646;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Sitana ponticeriana.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC   Sitana.
OX   NCBI_TaxID=118235;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A.;
RT   "Evolution and information content of the mitochondrial genomic
RT   structural features illustrated with acrodont lizards.";
RL   Syst. Biol. 49:257-277(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA   Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT   "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT   phylogenetics.";
RL   Syst. Biol. 49:233-256(2000).
DR   EMBL; AF128481; AAG00680.1; -.
KW   Mitochondrion.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1355 MW;  0A2D371E336411A0 CRC64;

  Query Match             75.0%;  Score 15;  DB 8;  Length 11;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       3 FITRW 7


RESULT 12
Q9G643
ID   Q9G643       PRELIMINARY;      PRT;    11 AA.
AC   Q9G643;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Calotes calotes.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC   Calotes.
OX   NCBI_TaxID=118093;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A.;
RT   "Evolution and information content of the mitochondrial genomic
RT   structural features illustrated with acrodont lizards.";
RL   Syst. Biol. 49:257-277(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA   Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT   "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT   phylogenetics.";
RL   Syst. Biol. 49:233-256(2000).
DR   EMBL; AF128482; AAG00683.1; -.
KW   Mitochondrion.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1373 MW;  BE2D371E336411A6 CRC64;

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  Best Local Similarity   40.0%;  Pred. No. 2.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       3 FMTRW 7


RESULT 13
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ID   Q9G640       PRELIMINARY;      PRT;    11 AA.
AC   Q9G640;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Calotes ceylonensis.
OG   Mitochondrion.
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC   Calotes.
OX   NCBI_TaxID=118094;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A.;
RT   "Evolution and information content of the mitochondrial genomic
RT   structural features illustrated with acrodont lizards.";
RL   Syst. Biol. 49:257-277(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA   Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT   "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT   phylogenetics.";
RL   Syst. Biol. 49:233-256(2000).
DR   EMBL; AF128483; AAG00686.1; -.
KW   Mitochondrion.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1355 MW;  4B2D371E336411A7 CRC64;

  Query Match             75.0%;  Score 15;  DB 8;  Length 11;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       3 FLTRW 7


RESULT 14
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ID   Q9G634      PRELIMINARY;      PRT;    11 AA.
AC   Q9G634;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Calotes liolepis.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC   Calotes.
OX   NCBI_TaxID=118096;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A.;
RT   "Evolution and information content of the mitochondrial genomic
RT   structural features illustrated with acrodont lizards.";
RL   Syst. Biol. 49:257-277(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA   Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT   "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT   phylogenetics.";
RL   Syst. Biol. 49:233-256(2000).
DR   EMBL; AF128485; AAG00692.1; -.
KW   Mitochondrion.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1355 MW;  4B2D371E336411A7 CRC64;

  Query Match             75.0%;  Score 15;  DB 8;  Length 11;
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Qy       1 FXXXW 5
           |   |
Db       3 FLTRW 7


RESULT 15
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ID   Q9G631      PRELIMINARY;      PRT;    11 AA.
AC   Q9G631;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Calotes nigrilabris.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC   Calotes.
OX   NCBI_TaxID=118098;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A.;
RT   "Evolution and information content of the mitochondrial genomic
RT   structural features illustrated with acrodont lizards.";
RL   Syst. Biol. 49:257-277(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA   Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT   "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT   phylogenetics.";
RL   Syst. Biol. 49:233-256(2000).
DR   EMBL; AF128486; AAG00695.1; -.
KW   Mitochondrion.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1355 MW;  4B2D371E336411A7 CRC64;

  Query Match             75.0%;  Score 15;  DB 8;  Length 11;
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  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       3 FLTRW 7


Search completed: January 29, 2003, 14:17:38
Job time : 29 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:12:43 ; Search time 34 Seconds
(without alignments)
19.596 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 289567

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	10	21	AAB10010	H. pylori beta-ure
2	17	85.0	10	22	AAB86058	H. pylori beta-ure
3	17	85.0	10	22	AAB86090	H. pylori beta-ure
4	17	85.0	13	22	AAE05735	Complementarity-de
5	17	85.0	14	22	AAM98088	Human peptide #136
6	17	85.0	15	17	AAR97874	Japan cedar pollen
7	17	85.0	15	17	AAR97875	Japan cedar pollen
8	17	85.0	15	19	AAW57758	Residues 16-30 of
9	17	85.0	19	23	AAE23038	Human thioredoxin,
10	17	85.0	20	19	AAW42165	T-cell epitope pep
11	17	85.0	20	22	AAG62999	Complementarity de
12	16	80.0	6	19	AAW76953	Fusion immunoglobu
13	16	80.0	8	20	AAY18082	Histamine/serotoni
14	16	80.0	9	20	AAY48085	Immunogenic peptid
15	16	80.0	9	22	AAE01057	Human secreted tum
16	16	80.0	9	23	ABP47522	N. meningitidis LO
17	16	80.0	10	6	AAP50792	Sequence of new go
18	16	80.0	10	9	AAP82754	Example of gonadot
19	16	80.0	10	21	AAB26393	Human CASB618 prot
20	16	80.0	10	21	AAB26399	Human CASB618 prot
21	16	80.0	10	22	ABB52440	Human API-186 tryp
22	16	80.0	10	22	AAB87239	Breast-cancer asso
23	16	80.0	10	22	AAB35295	Murine PSCA antibo
24	16	80.0	10	23	AAU72831	Anti-NKG2D hybrido
25	16	80.0	11	23	ABP47662	N. meningitidis LO
26	16	80.0	12	18	AAW32654	Human platelet gly
27	16	80.0	12	19	AAW71784	Mimotope capable o
28	16	80.0	12	22	AAB60021	Internalising pept
29	16	80.0	13	16	AAR70250	Pan DR-binding pep
30	16	80.0	13	18	AAW22121	Padre (pan-DR bind
31	16	80.0	13	19	AAW64575	Human Factor V pro
32	16	80.0	13	21	AAB36289	Promiscuous T help
33	16	80.0	13	21	AAY52558	Universal helper T
34	16	80.0	13	22	AAB73644	Pan-DR binding pep
35	16	80.0	13	22	AAB99710	Pan-DR-binding pep
36	16	80.0	13	22	AAB20154	PADRE peptide. Sy
37	16	80.0	13	23	AAU80293	Pan DR epitope pep
38	16	80.0	14	16	AAR72636	Cladosporium herba
39	16	80.0	14	22	AAM98495	Human peptide #177
40	16	80.0	14	22	AAM98808	Human peptide #208
41	16	80.0	15	15	AAR51379	Antigenic polypept
42	16	80.0	15	17	AAW07992	gp120 peptide 110.
43	16	80.0	15	19	AAW76978	Fusion immunoglobu
44	16	80.0	15	21	AAB29726	Ganglioside GM1-bi
45	16	80.0	15	21	AAB29164	Peptide #8. Unide

ALIGNMENTS

RESULT 1
AAB10010
ID AAB10010 standard; Protein; 10 AA.
XX
AC AAB10010;
XX
DT 01-NOV-2000 (first entry)
XX
DE H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2.
XX
KW Acid-resistant microorganism; detection; faecal; intestine; infection;
KW monoclonal antibody; heavy chain; complementarity determining region;
KW CDR; beta-urease.
XX
OS Unidentified.
XX
PN WO200026671-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-EP08212.
XX
PR 29-OCT-1998; 98EP-0120517.
PR 06-NOV-1998; 98EP-0120687.
XX
PA (CONN-) CONNEX GMBH.
XX
PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
PI Ringeis A;
XX
DR WPI; 2000-365747/31.
DR N-PSDB; AAA40166.
XX

PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
PT pylori, comprises reacting a faecal sample with two binding reagents for
PT antigens that survive intestinal passage -
XX
PS Claim 26; Page 22; 84pp; German.
XX
CC This invention describes a novel method for the detection of a mammalian
CC infection by an acid-resistant microorganism (A) by treating a faecal
CC sample with at least two different monoclonal antibodies (MAb) (or their
CC fragments or derivatives) or aptamers (collectively (I)) and detecting
CC formation of a complex (C) between (I) and the corresponding antigen of
CC (A). The first and second (I) bind to epitopes of different antigens
CC (Ag). These epitopes are present, after passage through the intestines,
CC in at least some mammals, and have either: (i) their native structure;
CC or (ii) a structure against which an antibody is produced by an animal
CC infected or immunized with (A), or its extract, lysate, derived protein
CC or fragment, or with a synthetic peptide. Practically all mammals display
CC at least one of the specified epitopes. The method is used to detect
CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,
CC M. tuberculosis, C. jejuni and C. pylori. (I) may also be used
CC therapeutically. The method is direct and non-invasive, and provides an
CC inexpensive and easily standardizable diagnosis, despite possible
CC degradation of antigens during passage through the intestines. This
CC sequence represents a fragment of a H. pylori beta-urease-binding
CC antibody heavy chain complementarity determining region CDR1 which is
CC used to illustrate the method of the invention.
XX
SQ Sequence 10 AA;

Query Match 85.0%; Score 17; DB 21; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FSTSW 8

RESULT 2
AAB86058
ID AAB86058 standard; Peptide; 10 AA.
XX
AC AAB86058;
XX
DT 17-JUL-2001 (first entry)
XX
DE H. pylori beta-urease derived antibody light chain CDR1 #1.
XX
KW Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;
KW antibacterial; complementarity determining region.
XX
OS Unidentified.
XX
PN WO200127613-A2.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-EP10058.
XX
PR 12-OCT-1999; 99EP-0120351.
PR 16-MAR-2000; 2000EP-0105592.
PR 31-MAR-2000; 2000EP-0107028.
PR 10-MAY-2000; 2000EP-0110110.
XX
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI Reiter C, Cullmann G, Heppner P, Ringeis A, Mueller H, Haindl E;
XX
DR WPI; 2001-282087/29.
DR N-PSDB; AAF88060.
XX

PT Detecting infections by acid-resistant microorganisms, particularly for
PT diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
PT sample -
XX
PS Claim 23; Page 17; 89pp; German.
XX
CC This invention describes a novel method for detecting, in a mammal,
CC infection by an acid-resistant microorganism (A) which comprises reacting
CC a fecal sample with: (i) a receptor (R) such that a complex is formed
CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part
CC complex is formed with Ag, and the formation of a complex detected. R are
CC specific for an Ag which, after passage through the intestines, at least
CC in some mammals, retains a native (or corresponding) structure against
CC which the mammal produces antibodies (when immunized or infected with
CC (A), or its extracts, lysates or derived proteins (or fragments) or
CC synthetic peptides). The products of the invention have antibacterial
CC activity. The method is used to diagnose infection by Helicobacter,
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the
CC progress of treatment. Receptors, particularly antibodies, directed
CC against Ag can be used therapeutically for treatment of infections. The
CC method requires only one R to provide a reasonably secure diagnosis
CC (although use of two R improves sensitivity), so is relatively
CC inexpensive and more easily standardized. Also it is direct,
CC non-invasive, suitable for automation and may indicate the stage of an
CC infection. This sequence represents a complementarity determining region
CC (CDR) from an antibody generated against a Helicobacter pylori antigen
CC (catalase or beta-urease) which is used to illustrate the method of the
CC invention.
XX
SQ Sequence 10 AA;

Query Match 85.0%; Score 17; DB 22; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FSTSW 8

RESULT 3
AAB86090
ID AAB86090 standard; Peptide; 10 AA.
XX
AC AAB86090;
XX
DT 17-JUL-2001 (first entry)
XX
DE H. pylori beta-urease derived antibody light chain CDR1 #1.
XX
KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
KW acid-resistant microorganism; complementarity determining region;
KW CDR; feces; heavy chain; light chain.
XX
OS Unidentified.
XX
PN WO200127612-A2.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-EP10057.
XX
PR 12-OCT-1999; 99EP-0120351.
PR 16-MAR-2000; 2000EP-0105592.
PR 31-MAR-2000; 2000EP-0107028.
PR 10-MAY-2000; 2000EP-0110110.
XX
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;
XX
DR WPI; 2001-282086/29.

DR N-PSDB; AAF88117.
XX
PT Detecting infections by acid-resistant microorganisms, particularly for
PT diagnosing Helicobacter pylori, comprises immunochromatographic
PT detection of antigen in feces -
XX
PS Claim 27; Page 27; 90pp; German.
XX
CC This invention describes a novel method for detecting infection by an
CC acid-resistant microorganism (A), in a mammal, using
CC immunochromatography. The method is used to diagnose infection by an
CC acid-resistant microorganism (A), in a mammal, such as Helicobacter,
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
CC inexpensive and non-invasive, and may indicate the stage of infection.
CC A test strip used in the method may include a filter to eliminate
CC particles present in the sample and only a single receptor provides a
CC reasonably secure diagnosis, with specificity and selectivity improved
CC by detecting several epitopes (of catalase) or different antigens
CC (catalase and beta-urease). The method can be automated. This sequence
CC represents a complementarity determining region (CDR) from an antibody
CC raised against the H. pylori catalase or beta-urease antigen which is
CC used to illustrate the method of the invention.
XX
SQ Sequence 10 AA;

Query Match 85.0%; Score 17; DB 22; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FSTSW 8

RESULT 4
AAE05735
ID AAE05735 standard; peptide; 13 AA.
XX
AC AAE05735;
XX
DT 24-SEP-2001 (first entry)
XX
DE Complementarity-determining region 3 (CDR3) of MoPhabs #7.
XX
KW CDR3; complementarity-determining region 3; monoclonal phage antibody;
KW MoPhabs; antigen.
XX
OS Synthetic.
XX
PN US6265150-B1.
XX
PD 24-JUL-2001.
XX
PF 26-MAY-1998; 98US-0085072.
XX
PR 07-JUN-1995; 95US-0483633.
PR 18-SEP-1997; 97US-0932892.
XX
PA (BECT) BECTON DICKINSON & CO.
PA (CRUC-) CRUCELL HOLLAND BV.
XX
PI Terstappen LW, Logtenberg T;
XX
DR WPI; 2001-463929/50.
XX
PT Obtaining a phage particle, useful for obtaining human antibodies
PT against known and novel surface antigens, by incubating a phage library
PT with target cells to allow binding of the antibody fragment to the
PT antigen -
XX
PS Example 6; Column 6; 6pp; English.
XX
CC The invention relates to a method of obtaining a phage particle
CC which has an antibody fragment directed against an antigen associated
CC with the surface of target cells in a heterogeneous cell population.
CC The method involves incubating a library of phage particles with the
CC target cells to allow binding of the antibody fragment expressed on
CC the surface of the phage particles to the antigen associated with
CC the target cells. The method is useful for obtaining human antibodies
CC against known and novel surface antigens in their native configuration,
CC expressed on phenotypically defined subpopulations of cells.
CC The present sequence is complementarity-determining region 3 (CDR3)
CC of monoclonal phage antibodies (MoPhabs) used in the exemplification
CC of the invention.
XX
SQ Sequence 13 AA;

Query Match 85.0%; Score 17; DB 22; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 6 FASSW 10

RESULT 5
AAM98088
ID AAM98088 standard; Peptide; 14 AA.
XX
AC AAM98088;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #1363 encoded by a SNP oligonucleotide.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Disclosure; Page 3967; 4143pp; English.
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.

```
CC   The oligonucleotides and the peptides encoded by them may be used in the
CC   prevention, diagnosis and treatment of diseases associated with
CC   inappropriate expression of the proteins listed above. Disorders that may
CC   be prevented, diagnosed and/or treated include multifactorial diseases
CC   with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC   arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
CC   and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC   brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC   system and an infection of pathogenic organisms.
XX
SQ   Sequence   14 AA;

  Query Match             85.0%;  Score 17;  DB 22;  Length 14;
  Best Local Similarity   40.0%;  Pred. No. 2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       6 FASTW 10


RESULT 6
AAR97874
ID   AAR97874 standard; peptide; 15 AA.
XX
AC   AAR97874;
XX
DT   16-AUG-1996  (first entry)
XX
DE   Japan cedar pollen mature allergen Cry j II amino acids 16-30.
XX
KW   Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
KW   Sugi pollinosis; diagnosis; treatment.
XX
OS   Cryptomeria japonica.
XX
PN   JP08047392-A.
XX
PD   20-FEB-1996.
XX
PF   07-NOV-1994;   94JP-0297840.
XX
PR   26-MAY-1994;   94JP-0134868.
PR   05-NOV-1993;   93JP-0276773.
XX
PA   (MEIP ) MEIJI MILK PROD CO LTD.
XX
DR   WPI; 1996-166249/17.
XX
PT   Japan cedar pollen allergen Cry j II epitope - comprises at least
PT   part of specified 460 amino acid protein
XX
PS   Claim 8; Fig 3; 17pp; Japanese.
XX
CC   AAR97871-R97960 are overlapping peptides used for the epitope mapping
CC   of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
CC   peptides of it are useful in the diagnosis, prevention and treatment
CC   of Sugi pollinosis, the allergic reaction to Japan cedar pollen.
CC   Significant regions of the allergen were identified using the
CC   overlapping peptides of the full epitope derived from a Cry j II
CC   antigen-specific T cell line. Amino acids 66-80 (AAR97884) and 186-200
CC   (R978908) of the full mature 460 amino acid allergen are the most
CC   allergenic of the 90 peptides tested.
XX
SQ   Sequence   15 AA;

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       9 FSTAW 13


RESULT 7
AAR97875
ID   AAR97875 standard; peptide; 15 AA.
XX
AC   AAR97875;
XX
DT   16-AUG-1996  (first entry)
XX
DE   Japan cedar pollen mature allergen Cry j II amino acids 21-35.
XX
KW   Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
KW   Sugi pollinosis; diagnosis; treatment.
XX
OS   Cryptomeria japonica.
XX
PN   JP08047392-A.
XX
PD   20-FEB-1996.
XX
PF   07-NOV-1994;   94JP-0297840.
XX
PR   26-MAY-1994;   94JP-0134868.
PR   05-NOV-1993;   93JP-0276773.
XX
PA   (MEIP ) MEIJI MILK PROD CO LTD.
XX
DR   WPI; 1996-166249/17.
XX
PT   Japan cedar pollen allergen Cry j II epitope - comprises at least
PT   part of specified 460 amino acid protein
XX
PS   Claim 8; Fig 3; 17pp; Japanese.
XX
CC   AAR97871-R97960 are overlapping peptides used for the epitope mapping
CC   of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
CC   peptides of it are useful in the diagnosis, prevention and treatment
CC   of Sugi pollinosis, the allergic reaction to Japan cedar pollen.
CC   Significant regions of the allergen were identified using the
CC   overlapping peptides of the full epitope derived from a Cry j II
CC   antigen-specific T cell line. Amino acids 66-80 (AAR97884) and 186-200
CC   (R978908) of the full mature 460 amino acid allergen are the most
CC   allergenic of the 90 peptides tested.
XX
SQ   Sequence   15 AA;

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSTAW 8


RESULT 8
AAW57758
ID   AAW57758 standard; peptide; 15 AA.
XX
AC   AAW57758;
XX
DT   17-SEP-1998  (first entry)
XX
DE   Residues 16-30 of Cry j 2.
XX
KW   Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;
KW   HLA class II molecule.
XX
OS   Cryptomeria japonica.
XX
PN   WO9820902-A1.
XX
```

PD 22-MAY-1998.
XX
PF 12-NOV-1997; 97WO-JP04129.
XX
PR 13-NOV-1996; 96JP-0302053.
XX
PA (MEIP) MEIJI MILK PROD CO LTD.
XX
PI Dairiki K, Kino K, Kume A, Sone T;
XX
DR WPI; 1998-297617/26.
XX
PT Peptides derived from Japanese cedar pollen antigens are
PT immunotherapeutic agents - useful for allergy treatment and typing
PT HLA class II molecules in allergy sufferers
XX
PS Claim 12; Page 29; 50pp; Japanese.
XX
CC This sequence represents residues 16-30 of the Cry j 2 protein, and
CC is a peptide of the invention. The peptides are derived from Japanese
CC cedar pollen antigens, and are used as immunotherapeutic agents in the
CC treatment of allergy. The peptides can be used for identification and
CC typing of the particular HLA class II molecules in an allergy sufferer,
CC and also for peptide immunotherapy of an allergy. Using these peptides
CC the immunotherapy can be targeted more specifically to the requirements
CC of the individual patient, allowing more effective treatment of an
CC allergy, including those patients for whom treatment with a conventional
CC immunotherapeutic agent is ineffective.
XX
SQ Sequence 15 AA;

Query Match 85.0%; Score 17; DB 19; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 9 FSTAW 13

RESULT 9
AAE23038
ID AAE23038 standard; peptide; 19 AA.
XX
AC AAE23038;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human thioredoxin, 47916 peptide.
XX
KW Human; thioredoxin; 22108; 47916; haematopoietic disorder; leukaemia;
KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;
KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;
KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;
KW cytostatic; carcinoma; cardiant; neuroprotective; antiinflammatory;
KW gene therapy; nootropic.
XX
OS Homo sapiens.
XX
PN WO200226803-A2.
XX
PD 04-APR-2002.
XX
PF 25-SEP-2001; 2001WO-US29967.
XX
PR 25-SEP-2000; 2000US-235049P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Bandaru R, Kapeller-Libermann R;
XX
DR WPI; 2002-416475/44.
XX
PT New human thioredoxin nucleic acid and polypeptide molecules,
PT designated 22108 and 47916, useful for diagnosing, preventing or
PT treating cancer (e.g. carcinoma), cardiovascular diseases (e.g. heart
PT failure) or brain disorders -
XX
PS Disclosure; Page 11; 124pp; English.
XX
CC The invention relates to human thioredoxin nucleic acid and polypeptide
CC molecules, designated 22108 and 47916. The compound that modulates the
CC activity or expression of 22108 and 47916 nucleic acid is useful for
CC treating or preventing a disorder characterised by aberrant activity of
CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting
CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The
CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,
CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,
CC metastatic or haematopoietic disorders (e.g.leukaemia), or cancers of
CC the lung, breast, thyroid, head neck, prostate or genito-urinary tract),
CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart
CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's
CC diseases). The thioredoxin DNA is also useful in gene therapy. The
CC present sequence is human thioredoxin, 47916 peptide.
XX
SQ Sequence 19 AA;

Query Match 85.0%; Score 17; DB 23; Length 19;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FSATW 8

RESULT 10
AAW42165
ID AAW42165 standard; peptide; 20 AA.
XX
AC AAW42165;
XX
DT 16-JUN-1998 (first entry)
XX
DE T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.
XX
KW Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;
KW diagnosis; allergy; spring tree pollen disease; pollinosis.
XX
OS Chamaeyparis obtusa.
XX
PN WO9747648-A1.
XX
PD 18-DEC-1997.
XX
PF 12-JUN-1997; 97WO-JP02031.
XX
PR 14-JUN-1996; 96JP-0153527.
XX
PA (MEIP) MEIJI MILK PROD CO LTD.
XX
PI Dairiki K, Kino K;
XX
DR WPI; 1998-052242/05.
XX
PT T-cell epitope peptide portion of Japanese cypress pollen antigens
PT Chao1 and Chao2 - used for diagnosis and treatment of spring tree
PT pollen disease
XX
PS Claim 2; Page 36; 71pp; Japanese.
XX
CC The present sequence represents a T-cell epitope peptide from Japanese
CC cypress pollen antigen Chao2. The present invention describes peptides
CC which correspond to the T-cell epitope sites on Japanese cypress pollen
CC antigens Chao1 and Chao2. The peptides can be used as a reagent for the
CC diagnosis of allergy to Japanese cypress pollen, and as an antigen in

```
CC   the treatment and prevention of spring tree pollen disease in which the
CC   pollinosis involves reactivity to Japanese cypress pollen.
XX
SQ   Sequence   20 AA;

  Query Match             85.0%;  Score 17;  DB 19;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 2.6e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       8 FATTW 12


RESULT 11
AAG62999
ID   AAG62999 standard; peptide; 20 AA.
XX
AC   AAG62999;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Complementarity determining region 3 (CDR3) of VH chain of clone G101.
XX
KW   Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW   endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW   transferrin receptor; neurological disease; Alzheimer's disease;
KW   prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS   Homo sapiens.
XX
PN   WO200144300-A2.
XX
PD   21-JUN-2001.
XX
PF   27-NOV-2000; 2000WO-GB04501.
XX
PR   13-DEC-1999;   99US-0170599.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Webster C,  Osbourn J,  Ward G,  Miller K;
XX
DR   WPI; 2001-398131/42.
XX
PT   Mixture or panel of antibodies for selecting specific binding members
PT   that cross the blood brain barrier, for use in delivering different
PT   molecules and treating neurological diseases
XX
PS   Claim 1; Page 76; 109pp; English.
XX
CC   AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC   of VL and VH chains of antibodies of the invention. The specification
CC   describes a mixture or panel of 5 different specific binding members,
CC   each comprising an antibody VH and/or VL variable domain and capable,
CC   when displayed on the surface of filamentous bacteriophage particles or
CC   in the case of a specific binding member comprising the D5 VH and/or VL
CC   variable domain when bound to human serum amyloid protein, to pass
CC   through a mammalian blood brain barrier (BBB). The panel is useful for
CC   the selection of specific binding members with a desired property such
CC   as ability to cross BBB, ability to bind endothelial cells or other brain
CC   cell antigen, ability to bind areas of inflammation in the brain or BBB
CC   breakdown or ability to bind intracellular adhesion molecules and to bind
CC   transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC   and treatment of human or animal body, including neurological diseases,
CC   such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC   epilepsy and traumatic brain injury and any diseases involving
CC   inflammation occurring within the brain or central nervous system.
XX
SQ   Sequence   20 AA;

  Query Match             85.0%;  Score 17;  DB 22;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 2.6e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSSSW 8


RESULT 12
AAW76953
ID   AAW76953 standard; peptide; 6 AA.
XX
AC   AAW76953;
XX
DT   25-JAN-1999  (first entry)
XX
DE   Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #93.
XX
KW   B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IgH;
KW   human immune deficiency virus; HIV; tolerance; treatment; therapy;
KW   prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;
KW   microbial infection; autoimmune disease; antibody; apoptosis;
KW   antiviral T cell immunity.
XX
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO9836087-A1.
XX
PD   20-AUG-1998.
XX
PF   13-FEB-1998;   98WO-US02766.
XX
PR   13-FEB-1997;   97US-0040581.
XX
PA   (AMNA-) AMERICAN NAT RED CROSS.
XX
PI   Scott D,  Zambidis E;
XX
DR   WPI; 1998-506315/43.
XX
PT   New fusion immunoglobulin heavy chain including gp120 epitopes and
PT   related complete antibodies - DNA, vectors and transformed cells,
PT   used to induce tolerance to the epitopes for treatment of human
PT   immune deficiency virus infection
XX
PS   Disclosure; Page 40; 154pp; English.
XX
CC   This sequence is an epitope used in the construction of a novel fusion
CC   immunoglobulin heavy chain (IgH) protein with a mammalian, especially
CC   human, IgH chain fused in frame at its N-terminus to one or more human
CC   immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or
CC   transfected cells are used to tolerise subjects to gp120 epitopes and to
CC   maintain this tolerance, particularly for treatment of HIV infection,
CC   optionally together with other therapeutic/prophylactic agents such as
CC   vaccines, chemotherapeutic agents and immune response modifiers. Such
CC   proteins can be used against other diseases where an immune response is
CC   deleterious, e.g. microbial infection, tumours or autoimmune disease.
CC   Induction of tolerance suppresses production of antibodies against gp120,
CC   so prevents or inhibits 'bystander' apoptosis of uninfected T cells that
CC   are bound to gp120 protein, maximising induction of protective antiviral
CC   T cell immunity.
XX
SQ   Sequence   6 AA;

  Query Match             80.0%;  Score 16;  DB 19;  Length 6;
  Best Local Similarity   40.0%;  Pred. No. 7.7e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       2 FNSTW 6
```

```
RESULT 13
AAY18082
ID   AAY18082 standard; peptide; 8 AA.
XX
AC   AAY18082;
XX
DT   06-AUG-1999  (first entry)
XX
DE   Histamine/serotonin cyclic binding peptide.
XX
KW   Histamine binding protein; serotonin binding compound; inflammation;
KW   gastric acid secretion; allergy; type I hypersensitivity reaction;
KW   asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy;
KW   drug allergy; abnormal blood pressure; psychological disorder; vaccine;
KW   respiratory disease; coronary heart disease; cellular growth regulator;
KW   tissue repair; blood-sucking ectoparasite; therapy.
XX
OS   Synthetic.
XX
PN   WO9927104-A1.
XX
PD   03-JUN-1999.
XX
PF   26-NOV-1998;   98WO-GB03530.
XX
PR   26-JUN-1998;   98GB-0013917.
PR   26-NOV-1997;   97GB-0025046.
XX
PA   (OXFO-) OXFORD VACS LTD.
XX
PI   Nuttall PA,  Paesen GC;
XX
DR   WPI; 1999-357841/30.
XX
PT   Histamine and serotonin binding compounds useful for the treatment
PT   of allergies
XX
PS   Claim 9; Page 43; 84pp; English.
XX
CC   This sequence is an example of a histamine or serotonin binding
CC   compound (A), of the invention. The compounds are useful for regulating
CC   the action of histamine and serotonin (in e.g. inflammation and gastric
CC   acid secretion), the detection, quantification and removal of histamine
CC   or serotonin (in animals, plants, cell cultures, food materials, or
CC   humans) and in the treatment of various diseases and allergies
CC   (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic
CC   rhinitis (hay fever), atopic dermatitis, insect bites and food and drug
CC   allergies, abnormal blood pressure, migraine, psychological disorders,
CC   respiratory disease, and coronary heart disease). Histamine may also be
CC   used to regulate cellular growth and tissue repair. The molecules may
CC   also be used as components of vaccines directed against blood-sucking
CC   ectoparasites.
XX
SQ   Sequence   8 AA;

  Query Match             80.0%;  Score 16;  DB 20;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 7.7e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
            |   |
Db       4 FAEAW 8


RESULT 14
AAY48085
ID   AAY48085 standard; Peptide; 9 AA.
XX
AC   AAY48085;
XX
DT   01-DEC-1999  (first entry)
XX
DE   Immunogenic peptide having a human leukocyte antigen binding motif #2696.
XX
KW   Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW   immune response; T cell activation; major histocompatibility complex;
KW   cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW   prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW   vaccine; immunisation.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9945954-A1.
XX
PD   16-SEP-1999.
XX
PF   13-MAR-1998;   98WO-US05039.
XX
PR   13-MAR-1998;   98WO-US05039.
XX
PA   (EPIM-) EPIMMUNE INC.
XX
PI   Sette A,  Kubo RT,  Sidney J,  Celis E,  Grey HM,  Southwood S;
XX
DR   WPI; 1999-551214/46.
XX
PT   New immunogenic peptides with HLA binding motif, useful in treatment
PT   and diagnosis of cancers and viral diseases
XX
PS   Claim 1; Page 136; 150pp; English.
XX
CC   AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC   having a human major histocompatibility complex (MHC) Class I (also
CC   known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC   peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC   HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC   response against the antigen from which the peptide is derived.
CC   Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC   normally induced by an antigen in the form of a peptide fragment bound
CC   to a HLA molecule, rather than the intact foreign antigen itself, and
CC   are particularly important in tumour rejection and in fighting viral
CC   infections. The peptides are therefore useful therapeutically to treat
CC   or prevent viral infections and cancers in mammals (especially humans)
CC   e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC   They can be administered as vaccines to elicit an immune response in
CC   individuals susceptible or otherwise at risk of viral infection or
CC   cancer, or used to treat chronic or acute conditions. They are also
CC   useful diagnostically, and can be used to induce a cytotoxic T cell
CC   response, by contacting a cytotoxic T cell with the peptide e.g. to
CC   produce CTLs ex vivo for infusion back into a patient. The
CC   polynucleotides encoding the immunogenic peptides are also useful
CC   therapeutically and for immunisation as above.
XX
SQ   Sequence   9 AA;

  Query Match             80.0%;  Score 16;  DB 20;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 7.7e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
            |   |
Db       5 FFSSW 9


RESULT 15
AAE01057
ID   AAE01057 standard; peptide; 9 AA.
XX
AC   AAE01057;
XX
DT   17-JUL-2001  (first entry)
XX
DE   Human secreted tumour antigen 36P6D5 peptide #10.
XX
KW   Human; 36P6D5 protein; secreted tumour antigen; therapy; cancer; kidney;
```

KW bladder; ovary; breast; pancreas; colon; lung; vaccine; cytostatic;
KW MHC; major histocompatibility complex; human leucocyte antigen; HLA-A2.
XX
OS Homo sapiens.
XX
PN WO200131015-A2.
XX
PD 03-MAY-2001.
XX
PF 30-OCT-2000; 2000WO-US29894.
XX
PR 28-OCT-1999; 99US-0162417.
XX
PA (UROG-) UROGENESYS INC.
XX
PI Raitano AB, Jakobovits A, Faris M, Afar DEH, Hubert RS;
PI Mitchell SC;
XX
DR WPI; 2001-308646/32.
XX
PT Detecting presence of cancer expressing 36P6D5 protein in individual by
PT comparing protein level in test sample to normal sample, where elevated
PT level of protein in test sample indicates presence of cancer -
XX
PS Claim 18; Page 91; 113pp; English.
XX
CC The present invention relates to a gene and its encoded secreted tumour
CC antigen, termed 36P6D5. These sequences are used for the diagnosis and
CC treatment of various cancers which express 36P6D5, such as cancers of
CC the kidney, bladder, ovary, breast, pancreas, colon and lungs. In normal
CC individuals 36P6D5 protein, is predominantly expressed in pancreas, with
CC lower levels of expression in prostate and small intestine. Vaccines
CC comprising immunogenic protein of 36P6D5 is useful for inhibiting the
CC development of prostate or colon cancer. Pharmaceutical composition
CC comprising 36P6D5 protein is useful for diagnosis and/or prognosis of
CC prostate cancer and other cancers, for modulating or inhibiting the
CC expression of 36P6D5 genes and/or translation of the 36P6D5 transcripts,
CC and as therapeutic agents. The present sequence is human 36P6D5 peptide.
CC This sequence binds to the human MHC (major histocompatibility complex)
CC class I molecule (human leucocyte antigen) HLA-A2 and its half time of
CC dissociation is 9.7
XX
SQ Sequence 9 AA;

Query Match 80.0%; Score 16; DB 22; Length 9;
Best Local Similarity 40.0%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 FXXXW 5
          |   |
Db      4 FRSSW 8
```

Search completed: January 29, 2003, 14:16:46
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:17:43 ; Search time 11 Seconds
(without alignments)
9.172 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 36068

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	80.0	7	9	US-10-046-922-48	Sequence 48, Appl
2	16	80.0	7	9	US-09-774-639-284	Sequence 284, App
3	16	80.0	9	9	US-10-046-922-59	Sequence 59, Appl
4	16	80.0	10	9	US-09-826-290-453	Sequence 453, App
5	16	80.0	13	9	US-09-949-375A-18	Sequence 18, Appl
6	16	80.0	13	9	US-09-785-215-19	Sequence 19, Appl
7	16	80.0	13	10	US-09-894-018-69	Sequence 69, Appl
8	16	80.0	15	10	US-09-205-658-284	Sequence 284, App
9	16	80.0	18	10	US-09-205-658-283	Sequence 283, App
10	16	80.0	18	10	US-09-205-658-285	Sequence 285, App
11	16	80.0	19	10	US-09-864-761-41546	Sequence 41546, A
12	16	80.0	20	10	US-09-812-528-19	Sequence 19, Appl
13	16	80.0	20	10	US-09-884-441-411	Sequence 411, App
14	16	80.0	20	10	US-09-884-441-412	Sequence 412, App
15	15	75.0	6	9	US-09-486-734A-34	Sequence 34, Appl
16	15	75.0	6	10	US-09-214-371-83	Sequence 83, Appl
17	15	75.0	6	10	US-09-732-384-4	Sequence 4, Appli
18	15	75.0	6	10	US-09-732-384-5	Sequence 5, Appli
19	15	75.0	6	12	US-10-155-059-1	Sequence 1, Appli
20	15	75.0	7	9	US-09-912-414-28	Sequence 28, Appl
21	15	75.0	7	10	US-09-096-749A-36	Sequence 36, Appl
22	15	75.0	8	8	US-08-424-550B-252	Sequence 252, App
23	15	75.0	8	10	US-09-214-371-12	Sequence 12, Appl
24	15	75.0	8	10	US-09-214-371-13	Sequence 13, Appl
25	15	75.0	8	10	US-09-214-371-21	Sequence 21, Appl
26	15	75.0	8	10	US-09-214-371-22	Sequence 22, Appl
27	15	75.0	8	10	US-09-214-371-46	Sequence 46, Appl
28	15	75.0	8	10	US-09-214-371-47	Sequence 47, Appl
29	15	75.0	8	10	US-09-214-371-48	Sequence 48, Appl
30	15	75.0	8	10	US-09-214-371-49	Sequence 49, Appl
31	15	75.0	8	10	US-09-214-371-52	Sequence 52, Appl
32	15	75.0	8	10	US-09-908-322-83	Sequence 83, Appl
33	15	75.0	9	1	US-08-821-739A-49	Sequence 49, Appl
34	15	75.0	9	1	US-08-821-739A-53	Sequence 53, Appl
35	15	75.0	9	9	US-09-771-415-16	Sequence 16, Appl
36	15	75.0	9	9	US-10-047-539-13	Sequence 13, Appl
37	15	75.0	9	10	US-09-214-371-37	Sequence 37, Appl
38	15	75.0	9	10	US-09-214-371-38	Sequence 38, Appl
39	15	75.0	9	10	US-09-764-304-12	Sequence 12, Appl
40	15	75.0	9	10	US-09-862-260A-13	Sequence 13, Appl
41	15	75.0	9	10	US-09-780-053-130	Sequence 130, App
42	15	75.0	10	9	US-09-826-290-390	Sequence 390, App
43	15	75.0	10	10	US-09-214-371-35	Sequence 35, Appl
44	15	75.0	10	10	US-09-214-371-36	Sequence 36, Appl
45	15	75.0	10	10	US-09-767-460-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-10-046-922-48
; Sequence 48, Application US/10046922
; Patent No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 7
; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-48

Query Match 80.0%; Score 16; DB 9; Length 7;
Best Local Similarity 40.0%; Pred. No. 9.9e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 3 FEAAW 7

RESULT 2
US-09-774-639-284
; Sequence 284, Application US/09774639
; Publication No. US20030003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371

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;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-774-639-284

  Query Match             80.0%;  Score 16;  DB 9;  Length 7;
  Best Local Similarity   40.0%;  Pred. No. 9.9e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       2 FGTSW 6


RESULT 3
US-10-046-922-59
; Sequence 59, Application US/10046922
; Patent No. US20020164667A1
; GENERAL INFORMATION:
;  APPLICANT: Alitalo, Kari
;  APPLICANT:  Koivunen, Erkki
;  APPLICANT:  Kubo, Hajime
;  TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
;  FILE REFERENCE: 28967/37084A
;  CURRENT APPLICATION NUMBER: US/10/046,922
;  CURRENT FILING DATE:  2002-01-15
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: peptide
US-10-046-922-59

  Query Match             80.0%;  Score 16;  DB 9;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 9.9e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FEAAW 8


RESULT 4
US-09-826-290-453
; Sequence 453, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
;  APPLICANT: Durham, L.Kathryn
;  APPLICANT:  Friedman, David L.
;  APPLICANT:  Herath, Herath Mudiyanselage Athula Chandrasiri
;  APPLICANT:  Kimmel, Lida H.
;  APPLICANT:  Parekh, Rajesh Bhikhu
;  APPLICANT:  Potter, David M.
;  APPLICANT:  Rohlff, Christian
;  APPLICANT:  Silber, B. Michael
;  APPLICANT:  Stiger, Thomas R.
;  APPLICANT:  Sunderland, P. Trey
;  APPLICANT:  Townsend, Robert Reid
;  APPLICANT:  White, Frost
;  APPLICANT:  Williams, Stephen A.
;  TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
;  TITLE OF INVENTION:  Uses Therefor, Including Diagnosis and Treatment of
;  TITLE OF INVENTION:  Alzheimer's Disease
;  FILE REFERENCE: 2572-1-001 N2
;  CURRENT APPLICATION NUMBER: US/09/826,290
;  CURRENT FILING DATE:  2001-04-30
;  PRIOR APPLICATION NUMBER: US 60/194,504
;  PRIOR FILING DATE: 2000-04-03
;  PRIOR APPLICATION NUMBER: US 60/253,647
;  PRIOR FILING DATE: 2000-11-28
;  NUMBER OF SEQ ID NOS: 492
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 453
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: homo sapien
US-09-826-290-453

  Query Match             80.0%;  Score 16;  DB 9;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 5e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FSGTW 5


RESULT 5
US-09-949-375A-18
; Sequence 18, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
;  APPLICANT: KLYSNER, Steen et al.
;  TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
;  FILE REFERENCE: 3631-0111P
;  CURRENT APPLICATION NUMBER: US/09/949,375A
;  CURRENT FILING DATE:  2002-01-18
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic amino acid sequence of SEQ ID NO: 17.
US-09-949-375A-18

  Query Match             80.0%;  Score 16;  DB 9;  Length 13;
  Best Local Similarity   40.0%;  Pred. No. 5.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       3 FVAAW 7


RESULT 6
US-09-785-215-19
; Sequence 19, Application US/09785215
; Publication No. US20020187157A1
; GENERAL INFORMATION:
;  APPLICANT: JENSEN, Martin Roland et al.
;  TITLE OF INVENTION: NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID
;  FILE REFERENCE: 3631-0107P
;  CURRENT APPLICATION NUMBER: US/09/785,215
;  CURRENT FILING DATE:  2001-02-20
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: artificial T-cell epitope capable of binding to a large portio
;   OTHER INFORMATION: of MHC Class II molecules in a variety of animals
US-09-785-215-19

  Query Match             80.0%;  Score 16;  DB 9;  Length 13;
  Best Local Similarity   40.0%;  Pred. No. 5.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
```

```
Db       3 FVAAW 7


RESULT 7
US-09-894-018-69
; Sequence 69, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
;  APPLICANT: EPIMMUNE, Inc.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Chestnut, Robert
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Baker, Denisw
;  APPLICANT:  Newman, Mark
;  APPLICANT:  Brown, David
;  TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
;  TITLE OF INVENTION:  MINIGENES AND PEPTIDES THEREBY
;  FILE REFERENCE: 39963-20033.00
;  CURRENT APPLICATION NUMBER: US/09/894,018
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: PCT/US00/35568
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: US 60/173,390
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: US 60/284,221
;  PRIOR FILING DATE: 2001-04-16
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 69
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PADRE sequence
US-09-894-018-69

  Query Match             80.0%;  Score 16;  DB 10;  Length 13;
  Best Local Similarity   40.0%;  Pred. No. 5.9e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       3 FVAAW 7


RESULT 8
US-09-205-658-284
; Sequence 284, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
;  APPLICANT: Ruvkun, Gary
;  APPLICANT: Ogg, Scott
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
;  TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
;  FILE REFERENCE: 00786/351004
;  CURRENT APPLICATION NUMBER: US/09/205,658
;  CURRENT FILING DATE: 1998-12-03
;  EARLIER APPLICATION NUMBER: 08/857,076
;  EARLIER FILING DATE: 1997-05-15
;  EARLIER APPLICATION NUMBER: 08/888,534
;  EARLIER FILING DATE: 1997-07-07
;  EARLIER APPLICATION NUMBER: US98/10080
;  EARLIER FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 328
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 284
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
US-09-205-658-284

  Query Match             80.0%;  Score 16;  DB 10;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 6.5e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       9 FSTRW 13


RESULT 9
US-09-205-658-283
; Sequence 283, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
;  APPLICANT: Ruvkun, Gary
;  APPLICANT: Ogg, Scott
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
;  TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
;  FILE REFERENCE: 00786/351004
;  CURRENT APPLICATION NUMBER: US/09/205,658
;  CURRENT FILING DATE: 1998-12-03
;  EARLIER APPLICATION NUMBER: 08/857,076
;  EARLIER FILING DATE: 1997-05-15
;  EARLIER APPLICATION NUMBER: 08/888,534
;  EARLIER FILING DATE: 1997-07-07
;  EARLIER APPLICATION NUMBER: US98/10080
;  EARLIER FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 328
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 283
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
US-09-205-658-283

  Query Match             80.0%;  Score 16;  DB 10;  Length 18;
  Best Local Similarity   40.0%;  Pred. No. 7.3e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      12 FSTRW 16


RESULT 10
US-09-205-658-285
; Sequence 285, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
;  APPLICANT: Ruvkun, Gary
;  APPLICANT: Ogg, Scott
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
;  TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
;  FILE REFERENCE: 00786/351004
;  CURRENT APPLICATION NUMBER: US/09/205,658
;  CURRENT FILING DATE: 1998-12-03
;  EARLIER APPLICATION NUMBER: 08/857,076
;  EARLIER FILING DATE: 1997-05-15
;  EARLIER APPLICATION NUMBER: 08/888,534
;  EARLIER FILING DATE: 1997-07-07
;  EARLIER APPLICATION NUMBER: US98/10080
;  EARLIER FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 328
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 285
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
US-09-205-658-285

  Query Match             80.0%;  Score 16;  DB 10;  Length 18;
  Best Local Similarity   40.0%;  Pred. No. 7.3e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
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          |   |
Db      12 FSTRW 16


RESULT 11
US-09-864-761-41546
; Sequence 41546, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41546
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL139352.8
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =   2
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL =   2
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
US-09-864-761-41546

  Query Match             80.0%;  Score 16;  DB 10;  Length 19;
  Best Local Similarity   40.0%;  Pred. No. 7.6e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      15 FSHSW 19


RESULT 12
US-09-812-528-19
; Sequence 19, Application US/09812528
; Patent No. US20010018210A1
; GENERAL INFORMATION:
;  APPLICANT: Bachovchin, William
;  APPLICANT:  Wallner, Barbara
;  TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN
;  TITLE OF INVENTION:  VITRO
;  FILE REFERENCE: I0248/7015
;  CURRENT APPLICATION NUMBER: US/09/812,528
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: US 60/060,306
;  PRIOR FILING DATE: 1997-09-29
;  PRIOR APPLICATION NUMBER: US 09/162,934
;  PRIOR FILING DATE: 1998-09-29
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-812-528-19

  Query Match             80.0%;  Score 16;  DB 10;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 7.8e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       3 FASRW 7


RESULT 13
US-09-884-441-411
; Sequence 411, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT:  Carter, Darrick
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 210121.462C7
;  CURRENT APPLICATION NUMBER: US/09/884,441
;  CURRENT FILING DATE:  2001-06-18
;  NUMBER OF SEQ ID NOS: 489
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 411
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-884-441-411

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  Best Local Similarity   40.0%;  Pred. No. 7.8e+02;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      11 FAISW 15


RESULT 14
US-09-884-441-412
; Sequence 412, Application US/09884441
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; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 412
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-412

Query Match 80.0%; Score 16; DB 10; Length 20;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FAISW 8

RESULT 15
US-09-486-734A-34
; Sequence 34, Application US/09486734A
; Patent No. US20020164732A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Marie-Christine
; APPLICANT: Clier, Florence
; APPLICANT: Erlich, S. Dusko
; APPLICANT: Gautier, Michel
; APPLICANT: Schouler, Catherine
; APPLICANT: Institut National de la Recherche Agronomique
; TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/M
; TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria
; FILE REFERENCE: 33339/196048
; CURRENT APPLICATION NUMBER: US/09/486,734A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/FR98/01873
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: FR 97/10885
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HsdS subunit
US-09-486-734A-34

Query Match 75.0%; Score 15; DB 9; Length 6;
Best Local Similarity 40.0%; Pred. No. 9.9e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 1 FADDW 5

Search completed: January 29, 2003, 14:21:23
Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:16:53 ; Search time 134 Seconds
(without alignments)
24.057 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 694069

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	9	24	US-10-072-419-3	Sequence 3, Appli
2	17	85.0	9	24	US-10-072-419-8	Sequence 8, Appli
3	17	85.0	10	22	US-09-842-776A-28	Sequence 28, Appl
4	17	85.0	10	24	US-10-089-452-36	Sequence 36, Appl
5	17	85.0	10	25	US-10-110-410-36	Sequence 36, Appl
6	17	85.0	11	24	US-10-072-419-37	Sequence 37, Appl
7	17	85.0	14	17	US-09-355-397C-36	Sequence 36, Appl
8	17	85.0	15	17	US-09-308-027-12	Sequence 12, Appl
9	17	85.0	15	17	US-09-308-027-88	Sequence 88, Appl
10	17	85.0	15	17	US-09-308-027A-12	Sequence 12, Appl
11	17	85.0	15	17	US-09-308-027A-88	Sequence 88, Appl
12	17	85.0	19	23	US-09-963-339-10	Sequence 10, Appl
13	17	85.0	19	25	US-10-145-586-59	Sequence 59, Appl
14	17	85.0	20	16	US-09-202-464-45	Sequence 45, Appl
15	17	85.0	20	16	US-09-240-203B-265	Sequence 265, App
16	17	85.0	20	16	US-09-240-203D-265	Sequence 265, App
17	16	80.0	6	1	PCT-US98-02766-155	Sequence 155, App
18	16	80.0	6	14	US-09-023-934-155	Sequence 155, App
19	16	80.0	7	16	US-09-244-112-284	Sequence 284, App
20	16	80.0	7	21	US-09-774-639-284	Sequence 284, App
21	16	80.0	7	23	US-09-969-730-267	Sequence 267, App
22	16	80.0	7	24	US-10-046-922-48	Sequence 48, Appl
23	16	80.0	8	1	PCT-US02-15590-51	Sequence 51, Appl
24	16	80.0	8	1	PCT-US02-15590-53	Sequence 53, Appl
25	16	80.0	8	1	PCT-US02-15590-55	Sequence 55, Appl
26	16	80.0	8	1	PCT-US02-15590-198	Sequence 198, App
27	16	80.0	8	1	PCT-US02-15590-200	Sequence 200, App
28	16	80.0	8	1	PCT-US02-15590-202	Sequence 202, App
29	16	80.0	8	1	PCT-US02-15590-204	Sequence 204, App
30	16	80.0	8	1	PCT-US02-15590-206	Sequence 206, App
31	16	80.0	8	1	PCT-US02-15590-225	Sequence 225, App
32	16	80.0	8	1	PCT-US02-15590-227	Sequence 227, App
33	16	80.0	8	1	PCT-US02-15590-229	Sequence 229, App
34	16	80.0	8	1	PCT-US02-15590-231	Sequence 231, App
35	16	80.0	8	1	PCT-US02-15590-233	Sequence 233, App
36	16	80.0	8	1	PCT-US02-15590-235	Sequence 235, App
37	16	80.0	8	1	PCT-US02-15590-237	Sequence 237, App
38	16	80.0	8	1	PCT-US02-15590-239	Sequence 239, App
39	16	80.0	8	19	US-09-555-296B-31	Sequence 31, Appl
40	16	80.0	8	24	US-10-072-419-4	Sequence 4, Appli
41	16	80.0	8	24	US-10-072-419-11	Sequence 11, Appl
42	16	80.0	8	24	US-10-072-419-15	Sequence 15, Appl
43	16	80.0	8	24	US-10-072-419-24	Sequence 24, Appl
44	16	80.0	8	24	US-10-072-419-25	Sequence 25, Appl
45	16	80.0	8	24	US-10-072-419-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-072-419-3
; Sequence 3, Application US/10072419
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in H
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-072-419-3

Query Match 85.0%; Score 17; DB 24; Length 9;
Best Local Similarity 40.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 4 FTSSW 8

RESULT 2
US-10-072-419-8

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; Sequence 8, Application US/10072419
; GENERAL INFORMATION:
;  APPLICANT: Schacter, Bernice
;  APPLICANT:  Schacter, Lee
;  TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Huma
;  FILE REFERENCE: 10739-1
;  CURRENT APPLICATION NUMBER: US/10/072,419
;  CURRENT FILING DATE:  2002-02-07
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Vanessa cardui
US-10-072-419-8

  Query Match             85.0%;  Score 17;  DB 24;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 4.2e+06;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FTSSW 8


RESULT 3
US-09-842-776A-28
; Sequence 28, Application US/09842776A
; GENERAL INFORMATION:
;  APPLICANT: CONNEX GMBH
;  TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
;  TITLE OF INVENTION:  IN THE STOOL
;  FILE REFERENCE: 41735
;  CURRENT APPLICATION NUMBER: US/09/842,776A
;  CURRENT FILING DATE:  2002-08-15
;  PRIOR APPLICATION NUMBER: PCT/EP99/08212
;  PRIOR FILING DATE: 1999-10-29
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Complementarity determining region (CDR1) of an
;   OTHER INFORMATION: antibody heavy chain directed to a beta-urease
;   OTHER INFORMATION: epitope (alternative sequence)
US-09-842-776A-28

  Query Match             85.0%;  Score 17;  DB 22;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.6e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FTSSW 8


RESULT 4
US-10-089-452-36
; Sequence 36, Application US/10089452
; GENERAL INFORMATION:
;  APPLICANT: Connex Gesellschaft zur Optimierung von Forschung und Entwicklung mbH
;  TITLE OF INVENTION: Improved Method for Detecting Acid Resistant Microorganisms in th
;  FILE REFERENCE: D 2394 PCT
;  CURRENT APPLICATION NUMBER: US/10/089,452
;  CURRENT FILING DATE:  2002-03-29
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: CDR
US-10-089-452-36

  Query Match             85.0%;  Score 17;  DB 24;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.6e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FTSSW 8


RESULT 5
US-10-110-410-36
; Sequence 36, Application US/10110410
; GENERAL INFORMATION:
;  APPLICANT: Connex Gesellschaft zur Optimierung von Forschung und Entwicklung mbH
;  TITLE OF INVENTION: Immunochromatographic Rapid Test for Detecting Acid Resistant
;  TITLE OF INVENTION:  Microorganisms in the Stool
;  FILE REFERENCE: D 1805 PCT
;  CURRENT APPLICATION NUMBER: US/10/110,410
;  CURRENT FILING DATE:  2002-04-12
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: CDR
US-10-110-410-36

  Query Match             85.0%;  Score 17;  DB 25;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.6e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FTSSW 8


RESULT 6
US-10-072-419-37
; Sequence 37, Application US/10072419
; GENERAL INFORMATION:
;  APPLICANT: Schacter, Bernice
;  APPLICANT:  Schacter, Lee
;  TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in H
;  FILE REFERENCE: 10739-1
;  CURRENT APPLICATION NUMBER: US/10/072,419
;  CURRENT FILING DATE:  2002-02-07
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Vanessa cardui
US-10-072-419-37

  Query Match             85.0%;  Score 17;  DB 24;  Length 11;
  Best Local Similarity   40.0%;  Pred. No. 1.7e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FTSSW 8


RESULT 7
US-09-355-397C-36
; Sequence 36, Application US/09355397C
```

```
; GENERAL INFORMATION:
;  APPLICANT: Spyrou, Giannis
;  TITLE OF INVENTION: Mammalian Thioredoxin
;  FILE REFERENCE: 102043-100
;  CURRENT APPLICATION NUMBER: US/09/355,397C
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: PCT/GB98/00263
;  PRIOR FILING DATE: 1998-01-28
;  PRIOR APPLICATION NUMBER: GB 9701710.7
;  PRIOR FILING DATE: 1997-01-28
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: mammal
US-09-355-397C-36

  Query Match             85.0%;  Score 17;  DB 17;  Length 14;
  Best Local Similarity   40.0%;  Pred. No. 2e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       5 FSATW 9


RESULT 8
US-09-308-027-12
; Sequence 12, Application US/09308027
; GENERAL INFORMATION:
;  APPLICANT:  Sone, Toshio
;  APPLICANT:  Kume, Akinori
;  APPLICANT:  Dairiki, Kazuo
;  APPLICANT:  Kino, Koshuke
;  TITLE OF INVENTION:  PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
;  FILE REFERENCE:  06501/031001
;  CURRENT APPLICATION NUMBER: US/09/308,027
;  CURRENT FILING DATE:  1999-08-16
;  PRIOR APPLICATION NUMBER:  PCT/JP97/04129
;  PRIOR FILING DATE:  1997-11-12
;  PRIOR APPLICATION NUMBER:  JP 8/302053
;  PRIOR FILING DATE:  1996-11-13
;  NUMBER OF SEQ ID NOS:  146
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Cryptomeria
US-09-308-027-12

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       9 FSTAW 13


RESULT 9
US-09-308-027-88
; Sequence 88, Application US/09308027
; GENERAL INFORMATION:
;  APPLICANT:  Sone, Toshio
;  APPLICANT:  Kume, Akinori
;  APPLICANT:  Dairiki, Kazuo
;  APPLICANT:  Kino, Koshuke
;  TITLE OF INVENTION:  PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
;  FILE REFERENCE:  06501/031001
;  CURRENT APPLICATION NUMBER: US/09/308,027
;  CURRENT FILING DATE:  1999-08-16
;  PRIOR APPLICATION NUMBER:  PCT/JP97/04129
;  PRIOR FILING DATE:  1997-11-12
;  PRIOR APPLICATION NUMBER:  JP 8/302053
;  PRIOR FILING DATE:  1996-11-13
;  NUMBER OF SEQ ID NOS:  146
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 88
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Cryptomeria
US-09-308-027-88

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSTAW 8


RESULT 10
US-09-308-027A-12
; Sequence 12, Application US/09308027A
; GENERAL INFORMATION:
;  APPLICANT: Sone, Toshio
;  APPLICANT:  Kume, Akinori
;  APPLICANT:  Dairiki, Kazuo
;  APPLICANT:  Kino, Kohsuke
;  TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
;  FILE REFERENCE: 06501/031001
;  CURRENT APPLICATION NUMBER: US/09/308,027A
;  CURRENT FILING DATE:  1999-08-16
;  PRIOR APPLICATION NUMBER: PCT/JP97/04129
;  PRIOR FILING DATE: 1997-11-12
;  PRIOR APPLICATION NUMBER: JP 8/302053
;  PRIOR FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Cryptomeria
US-09-308-027A-12

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       9 FSTAW 13


RESULT 11
US-09-308-027A-88
; Sequence 88, Application US/09308027A
; GENERAL INFORMATION:
;  APPLICANT: Sone, Toshio
;  APPLICANT:  Kume, Akinori
;  APPLICANT:  Dairiki, Kazuo
;  APPLICANT:  Kino, Kohsuke
;  TITLE OF INVENTION: PEPTIDE-BASED IMMUNOTHERAPEUTIC AGENT
;  FILE REFERENCE: 06501/031001
;  CURRENT APPLICATION NUMBER: US/09/308,027A
;  CURRENT FILING DATE:  1999-08-16
;  PRIOR APPLICATION NUMBER: PCT/JP97/04129
;  PRIOR FILING DATE: 1997-11-12
;  PRIOR APPLICATION NUMBER: JP 8/302053
;  PRIOR FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 88
;   LENGTH: 15
```

```
;   TYPE: PRT
;   ORGANISM: Cryptomeria
US-09-308-027A-88

  Query Match             85.0%;  Score 17;  DB 17;  Length 15;
  Best Local Similarity   40.0%;  Pred. No. 2.1e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSTAW 8


RESULT 12
US-09-963-339-10
; Sequence 10, Application US/09963339
; GENERAL INFORMATION:
;  APPLICANT: Bandaru, Rajasekhar
;  TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
;  TITLE OF INVENTION:  FAMILY MEMBERS AND USES THEREOF
;  FILE REFERENCE: 10448-090001
;  CURRENT APPLICATION NUMBER: US/09/963,339
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 60/235,049
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-963-339-10

  Query Match             85.0%;  Score 17;  DB 23;  Length 19;
  Best Local Similarity   40.0%;  Pred. No. 2.4e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSATW 8


RESULT 13
US-10-145-586-59
; Sequence 59, Application US/10145586
; GENERAL INFORMATION:
;  APPLICANT: Alexandra Glucksmann, Maria
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  M. Galvin, Katherine
;  APPLICANT:  Weich, Nadine
;  APPLICANT:  Curtis, Rory A.J.
;  APPLICANT:  Bandaru, Rajasekhar
;  APPLICANT:  Kapeller-Libermann, Rosana
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
;  TITLE OF INVENTION:  HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
;  TITLE OF INVENTION:  REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
;  FILE REFERENCE: 10448-188001
;  CURRENT APPLICATION NUMBER: US/10/145,586
;  CURRENT FILING DATE:  2002-05-14
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 95
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-145-586-59

  Query Match             85.0%;  Score 17;  DB 25;  Length 19;
  Best Local Similarity   40.0%;  Pred. No. 2.4e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSATW 8


RESULT 14
US-09-202-464-45
; Sequence 45, Application US/09202464
;   GENERAL INFORMATION:
;        APPLICANT: Kino, Kohsuke
;                   Dairiki, Kazuo
;        TITLE OF INVENTION: T-CELL EPITOPE PEPTIDES
;        NUMBER OF SEQUENCES: 90
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 225 Franklin Street
;             CITY: Boston
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02110-2804
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/202,464
;             FILING DATE: 14-Dec-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: WO JP97/02031
;             FILING DATE: 12-JUN-1997
;             APPLICATION NUMBER: JP 8/153527
;             FILING DATE: 14-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Fraser, Ph.D., J.D., Janis K.
;             REGISTRATION NUMBER: 34,819
;             REFERENCE/DOCKET NUMBER: 06501-024001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617/542-5070
;             TELEFAX: 617/542-8906
;   INFORMATION FOR SEQ ID NO: 45:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-202-464-45

  Query Match             85.0%;  Score 17;  DB 16;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       8 FATTW 12


RESULT 15
US-09-240-203B-265
; Sequence 265, Application US/09240203B
;   GENERAL INFORMATION:
;        APPLICANT: Griffith, Irwin J.;
;                   Pollock, Joanne;
;                   Bond, Julian F.;
;                   Garman, Richard D;
;                   Kuo, Mei-Chang;
;                   Powers, Steven P.;
;                   Exley, Mark A.;
;                   Chen, Xian;
;                   Shaked, Ze'ev
;        TITLE OF INVENTION: Allergenic Proteins And Peptides From
;                            Japanese Cedar Pollen
;        NUMBER OF SEQUENCES: 265
```

```
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Lahive & Cockfield, LLP
;            STREET: 28 State St
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/240,203B
;            FILING DATE: 22-Jun-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/350,225
;            FILING DATE: December 6, 1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Amy E. Mandragouras, Esq.
;            REGISTRATION NUMBER: 36,207
;            REFERENCE/DOCKET NUMBER: 1MI-028CD2CCPA2
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617) 227-7400
;            TELEFAX: (617) 742-4214
;   INFORMATION FOR SEQ ID NO: 265:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 20 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       FRAGMENT TYPE: internal
;       SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-240-203B-265

  Query Match             85.0%;  Score 17;  DB 16;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 2.5e+04;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db      12 FSTAW 16


Search completed: January 29, 2003, 14:20:41
Job time : 135 secs
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:17:08 ; Search time 18 Seconds
(without alignments)
21.950 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 396018 seqs, 79020188 residues

Total number of hits satisfying chosen parameters: 139460

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	80.0	8	5	US-09-641-528-44	Sequence 44, Appl
2	16	80.0	8	5	US-09-641-528-734	Sequence 734, App
3	16	80.0	8	5	US-09-641-528-1054	Sequence 1054, Ap
4	16	80.0	8	5	US-09-641-528-20273	Sequence 20273, A
5	16	80.0	8	5	US-09-641-528-20303	Sequence 20303, A
6	16	80.0	8	5	US-09-641-528-21722	Sequence 21722, A
7	16	80.0	8	5	US-09-641-528-21757	Sequence 21757, A
8	16	80.0	8	5	US-09-641-528-22468	Sequence 22468, A
9	16	80.0	8	5	US-09-641-528-22509	Sequence 22509, A
10	16	80.0	8	5	US-09-641-528-31337	Sequence 31337, A
11	16	80.0	8	5	US-09-641-528-34368	Sequence 34368, A
12	16	80.0	8	5	US-09-641-528-35881	Sequence 35881, A
13	16	80.0	8	5	US-09-641-528-39670	Sequence 39670, A
14	16	80.0	8	5	US-09-641-528-41710	Sequence 41710, A
15	16	80.0	8	5	US-09-641-528-42699	Sequence 42699, A
16	16	80.0	8	5	US-09-641-528A-44	Sequence 44, Appl
17	16	80.0	8	5	US-09-641-528A-734	Sequence 734, App
18	16	80.0	8	5	US-09-641-528A-1054	Sequence 1054, Ap
19	16	80.0	8	5	US-09-641-528A-20273	Sequence 20273, A
20	16	80.0	8	5	US-09-641-528A-20303	Sequence 20303, A
21	16	80.0	8	5	US-09-641-528A-21722	Sequence 21722, A
22	16	80.0	8	5	US-09-641-528A-21757	Sequence 21757, A
23	16	80.0	8	5	US-09-641-528A-22468	Sequence 22468, A
24	16	80.0	8	5	US-09-641-528A-22509	Sequence 22509, A
25	16	80.0	8	5	US-09-641-528A-31337	Sequence 31337, A
26	16	80.0	8	5	US-09-641-528A-34368	Sequence 34368, A
27	16	80.0	8	5	US-09-641-528A-35881	Sequence 35881, A
28	16	80.0	8	5	US-09-641-528A-39670	Sequence 39670, A
29	16	80.0	8	5	US-09-641-528A-41710	Sequence 41710, A
30	16	80.0	8	5	US-09-641-528A-42699	Sequence 42699, A
31	16	80.0	9	5	US-09-641-528-11581	Sequence 11581, A
32	16	80.0	9	5	US-09-641-528-13540	Sequence 13540, A
33	16	80.0	9	5	US-09-641-528-14470	Sequence 14470, A
34	16	80.0	9	5	US-09-641-528-17935	Sequence 17935, A
35	16	80.0	9	5	US-09-641-528-18786	Sequence 18786, A
36	16	80.0	9	5	US-09-641-528-19183	Sequence 19183, A
37	16	80.0	9	5	US-09-641-528-31569	Sequence 31569, A
38	16	80.0	9	5	US-09-641-528-34605	Sequence 34605, A
39	16	80.0	9	5	US-09-641-528-36102	Sequence 36102, A
40	16	80.0	9	5	US-09-641-528-39826	Sequence 39826, A
41	16	80.0	9	5	US-09-641-528-41874	Sequence 41874, A
42	16	80.0	9	5	US-09-641-528-42842	Sequence 42842, A
43	16	80.0	9	5	US-09-641-528-45197	Sequence 45197, A
44	16	80.0	9	5	US-09-641-528-45626	Sequence 45626, A
45	16	80.0	9	5	US-09-641-528-45830	Sequence 45830, A

ALIGNMENTS

RESULT 1
US-09-641-528-44
; Sequence 44, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-44

Query Match 80.0%; Score 16; DB 5; Length 8;
Best Local Similarity 40.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 FXXXW 5
           |   |
Db       4 FSRTW 8
```

RESULT 2
US-09-641-528-734
; Sequence 734, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001

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;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 734
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-734

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSRTW 8


RESULT 3
US-09-641-528-1054
; Sequence 1054, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1054
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-1054

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSRTW 8


RESULT 4
US-09-641-528-20273
; Sequence 20273, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20273
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-20273

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FSRTW 5


RESULT 5
US-09-641-528-20303
; Sequence 20303, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20303
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-20303

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSRTW 8


RESULT 6
US-09-641-528-21722
; Sequence 21722, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
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;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21722
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-21722

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
            |   |
Db       1 FSRTW 5


RESULT 7
US-09-641-528-21757
; Sequence 21757, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21757
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-21757

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
            |   |
Db       4 FSRTW 8


RESULT 8
US-09-641-528-22468
; Sequence 22468, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22468
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-22468

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
            |   |
Db       1 FSRTW 5


RESULT 9
US-09-641-528-22509
; Sequence 22509, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22509
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-22509

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
            |   |
Db       4 FSRTW 8


RESULT 10
US-09-641-528-31337
; Sequence 31337, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
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;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31337
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-31337

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       2 FSRTW 6


RESULT 11
US-09-641-528-34368
; Sequence 34368, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34368
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-34368

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       2 FSRTW 6


RESULT 12
US-09-641-528-35881
; Sequence 35881, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35881
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-35881

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       2 FSRTW 6


RESULT 13
US-09-641-528-39670
; Sequence 39670, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39670
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-39670

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       2 FSRTW 6


RESULT 14
US-09-641-528-41710
; Sequence 41710, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 41710
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-41710

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       2 FSRTW 6


RESULT 15
US-09-641-528-42699
; Sequence 42699, Application US/09641528
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51504
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42699
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-42699

  Query Match             80.0%;  Score 16;  DB 5;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 3e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       2 FSRTW 6


Search completed: January 29, 2003, 14:21:05
Job time : 18 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:16:08 ; Search time 14 Seconds
(without alignments)
10.508 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 132970

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	85.0	13	4	US-09-085-072-7	Sequence 7, Appli
2	16	80.0	6	1	US-07-920-519-10	Sequence 10, Appl
3	16	80.0	6	1	US-08-086-410-7	Sequence 7, Appli
4	16	80.0	6	1	US-08-314-586-10	Sequence 10, Appl
5	16	80.0	10	1	US-08-208-886C-87	Sequence 87, Appl
6	16	80.0	10	1	US-08-704-744-89	Sequence 89, Appl
7	16	80.0	10	1	US-08-469-557-68	Sequence 68, Appl
8	16	80.0	10	2	US-08-290-793B-68	Sequence 68, Appl
9	16	80.0	11	1	US-08-277-660A-16	Sequence 16, Appl
10	16	80.0	11	1	US-08-277-660A-17	Sequence 17, Appl
11	16	80.0	11	1	US-08-424-957-29	Sequence 29, Appl
12	16	80.0	11	1	US-08-424-957-30	Sequence 30, Appl
13	16	80.0	11	4	US-09-035-686-29	Sequence 29, Appl
14	16	80.0	11	4	US-09-035-686-30	Sequence 30, Appl
15	16	80.0	12	2	US-08-406-330-32	Sequence 32, Appl
16	16	80.0	12	2	US-08-556-597-32	Sequence 32, Appl
17	16	80.0	13	1	US-08-305-871A-23	Sequence 23, Appl
18	16	80.0	13	3	US-08-912-560-11	Sequence 11, Appl
19	16	80.0	13	4	US-08-788-822A-27	Sequence 27, Appl
20	16	80.0	13	6	5185431-25	Patent No. 5185431
21	16	80.0	15	1	US-08-218-025A-139	Sequence 139, App
22	16	80.0	15	4	US-08-847-844A-22	Sequence 22, Appl
23	16	80.0	15	5	PCT-US93-08699-1	Sequence 1, Appli
24	16	80.0	16	4	US-09-330-914A-11	Sequence 11, Appl
25	16	80.0	17	1	US-08-218-025A-115	Sequence 115, App
26	16	80.0	17	2	US-08-746-283-7	Sequence 7, Appli
27	16	80.0	17	2	US-08-746-257A-5	Sequence 5, Appli
28	16	80.0	17	3	US-08-987-743-11	Sequence 11, Appl
29	16	80.0	18	2	US-08-934-915-125	Sequence 125, App
30	16	80.0	18	3	US-08-513-968-40	Sequence 40, Appl
31	16	80.0	18	4	US-09-025-769B-249	Sequence 249, App
32	16	80.0	20	1	US-08-218-025A-64	Sequence 64, Appl
33	16	80.0	20	1	US-08-218-025A-65	Sequence 65, Appl
34	16	80.0	20	2	US-08-493-235-31	Sequence 31, Appl
35	16	80.0	20	4	US-09-162-934-19	Sequence 19, Appl
36	15	75.0	6	1	US-08-277-660A-2	Sequence 2, Appli
37	15	75.0	6	1	US-08-277-660A-3	Sequence 3, Appli
38	15	75.0	6	1	US-08-424-957-2	Sequence 2, Appli
39	15	75.0	6	1	US-08-424-957-3	Sequence 3, Appli
40	15	75.0	6	1	US-08-424-957-6	Sequence 6, Appli
41	15	75.0	6	4	US-09-035-686-2	Sequence 2, Appli
42	15	75.0	6	4	US-09-035-686-3	Sequence 3, Appli
43	15	75.0	6	4	US-09-035-686-6	Sequence 6, Appli
44	15	75.0	6	4	US-09-081-975-1	Sequence 1, Appli
45	15	75.0	7	1	US-08-358-160-189	Sequence 189, App

ALIGNMENTS

RESULT 1
US-09-085-072-7
; Sequence 7, Application US/09085072
; Patent No. 6265150
; GENERAL INFORMATION:
; APPLICANT: L. Terstappen et al.
; TITLE OF INVENTION: PHAGE ANTIBODIES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,072
; FILING DATE: 26-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: 890-2 FWC/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-085-072-7

Query Match 85.0%; Score 17; DB 4; Length 13;
Best Local Similarity 40.0%; Pred. No. 8.7e+02;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 6 FASSW 10

RESULT 2

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US-07-920-519-10
; Sequence 10, Application US/07920519
; Patent No. 5382518
;  GENERAL INFORMATION:
;     APPLICANT:  CAPUT, DANIEL
;     APPLICANT:  FERRARA, PASCUAL
;     APPLICANT:  GUILLEMOT, JEAN-CLAUDE
;     APPLICANT:  KAGHAD, MOURAD
;     APPLICANT:  LEGOUX, RICHARD
;     APPLICANT:  LOISON, GERARD
;     APPLICANT:  LARBRE, ELIZABETH
;     APPLICANT:  LUPKER, JOHANNES
;     APPLICANT:  LEPLATOIS, PASCUAL
;     APPLICANT:  SALOME, MARK
;     TITLE OF INVENTION:  URATE OXIDASE ACTIVITY PROTEIN,
;     TITLE OF INVENTION:  RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
;     TITLE OF INVENTION:  MICRO-ORGANISMS AND TRANSFORMED CELLS
;     NUMBER OF SEQUENCES:  36
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  1800 Diagonal Road, Suite 500
;       CITY:  Alexandria
;       STATE:  Virginia
;       COUNTRY:  USA
;       ZIP:  22313-0299
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/920,519
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/659,408
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BENT, Stephen A.
;       REGISTRATION NUMBER:  29,768
;       REFERENCE/DOCKET NUMBER:  16781/276 BEDL
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703)836-9300
;       TELEFAX:  (703)683-4109
;       TELEX:  899149
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     IMMEDIATE SOURCE:
;       CLONE:  Hydrolysis product T 23
US-07-920-519-10

  Query Match             80.0%;  Score 16;  DB 1;  Length 6;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FDATW 5


RESULT 3
US-08-086-410-7
; Sequence 7, Application US/08086410
; Patent No. 5407822
;  GENERAL INFORMATION:
;     APPLICANT:  LEPLATOIS, Pascal
;     APPLICANT:  LOISON, Gerard
;     APPLICANT:  PESSEGUE, Bernard
;     APPLICANT:  SHIRE, David
;     TITLE OF INVENTION:  Artificial promoter for the expression
;     TITLE OF INVENTION:  of proteins in yeast
;     NUMBER OF SEQUENCES:  37
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  FOLEY & LARDNER
;       STREET:  King Street Station,Suite 500,1800 Diagonal
;       STREET:  Road,PO Box 299
;       CITY:  ALEXANDRIA
;       STATE:  VIRGINIA
;       COUNTRY:  USA
;       ZIP:  22313-0299
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/086,410
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/768,083
;       FILING DATE:  02-OCT-1991
;       APPLICATION NUMBER:  FR 89 17467
;       FILING DATE:  29-DEC-1989
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SAXE, Bernhard D
;       REGISTRATION NUMBER:  28,665
;       REFERENCE/DOCKET NUMBER:  16781/318
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 836-9300
;       TELEFAX:  (703) 683-4109
;       TELEX:  899149
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       CLONE:  hydrolysis product T23
US-08-086-410-7

  Query Match             80.0%;  Score 16;  DB 1;  Length 6;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FDATW 5


RESULT 4
US-08-314-586-10
; Sequence 10, Application US/08314586
; Patent No. 5541098
;  GENERAL INFORMATION:
;     APPLICANT:  CAPUT, DANIEL
;     APPLICANT:  FERRARA, PASCUAL
;     APPLICANT:  GUILLEMOT, JEAN-CLAUDE
;     APPLICANT:  KAGHAD, MOURAD
;     APPLICANT:  LEGOUX, RICHARD
;     APPLICANT:  LOISON, GERARD
;     APPLICANT:  LARBRE, ELIZABETH
;     APPLICANT:  LUPKER, JOHANNES
;     APPLICANT:  LEPLATOIS, PASCUAL
;     APPLICANT:  SALOME, MARK
;     APPLICANT:  LAURENT, PATRICK
;     TITLE OF INVENTION:  URATE OXIDASE ACTIVITY PROTEIN,
;     TITLE OF INVENTION:  RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
;     TITLE OF INVENTION:  MICROORGANISMS AND TRANSFORMED CELLS
```

```
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/314,586
;      FILING DATE:  28-SEP-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/659,408
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16781/509/BEDL
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  Hydrolysis product T 23
US-08-314-586-10

  Query Match             80.0%;  Score 16;  DB 1;  Length 6;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FDATW 5


RESULT 5
US-08-208-886C-87
; Sequence 87, Application US/08208886C
; Patent No. 5597710
;  GENERAL INFORMATION:
;    APPLICANT:  Dalie, Barbara
;    APPLICANT:  Miller, Kenneth
;    APPLICANT:  Murgolo, Nicholas
;    APPLICANT:  Tindall, Stephen
;    TITLE OF INVENTION:  Humanized Monoclonal Antibodies Against Human Interleukin-4
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schering-Plough Corporation
;      STREET:  2000 Galloping Hill Road
;      CITY:  Kenilworth
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07033-0530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/208,886C
;      FILING DATE:  March 10, 1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foulke, Cynthia L.
;      REGISTRATION NUMBER:  32,364
;      REFERENCE/DOCKET NUMBER:  JB0429
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 298 2987
;      TELEFAX:  908 298 5388
;  INFORMATION FOR SEQ ID NO:  87:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-208-886C-87

  Query Match             80.0%;  Score 16;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSSYW 8


RESULT 6
US-08-704-744-89
; Sequence 89, Application US/08704744
; Patent No. 5705154
;  GENERAL INFORMATION:
;    APPLICANT:  Dalie, Barbara
;    APPLICANT:  Miller, Kenneth
;    APPLICANT:  Murgolo, Nicholas
;    APPLICANT:  Tindall, Stephen
;    TITLE OF INVENTION:  Humanized Monoclonal Antibodies Against Human Interleukin-4
;    NUMBER OF SEQUENCES:  90
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schering-Plough Corporation
;      STREET:  2000 Galloping Hill Road
;      CITY:  Kenilworth
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07033-0530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.5.3
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/704,744
;      FILING DATE:  06-SEPT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/208886
;      FILING DATE:  10-MAR-1994
;      APPLICATION NUMBER:  PCT/US/95/02400
;      FILING DATE:  08-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foulke, Cynthia L.
;      REGISTRATION NUMBER:  32,364
;      REFERENCE/DOCKET NUMBER:  JB0429K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 298-2987
;      TELEFAX:  (908) 298-5388
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
```

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;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-704-744-89

  Query Match             80.0%;  Score 16;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSSYW 8


RESULT 7
US-08-469-557-68
; Sequence 68, Application US/08469557
; Patent No. 5770403
;  GENERAL INFORMATION:
;     APPLICANT:  Dalie, Barbara
;     APPLICANT:  Le, Hung
;     APPLICANT:  Miller, Kenneth
;     APPLICANT:  Murgolo, Nicholas
;     APPLICANT:  Nguyen, Hanh
;     APPLICANT:  Tindall, Stephen
;     APPLICANT:  Zavodny, Paul
;     TITLE OF INVENTION:  Cloning and Expression of
;     TITLE OF INVENTION:  Humanized Monoclonal Antibodies
;     TITLE OF INVENTION:  Against Human Interleukin-4
;     NUMBER OF SEQUENCES:  69
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Schering-Plough Corporation
;       STREET:  2000 Galloping Hill Road
;       CITY:  Kenilworth
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07033-0530
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  Apple Macintosh
;       OPERATING SYSTEM:  Macintosh 6.0.5
;       SOFTWARE:  Microsoft Word 5.1A
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/469,557
;       FILING DATE:  06-JUN-1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/290,793
;       FILING DATE:  August 16, 1994
;       APPLICATION NUMBER:  PCT/US93/01301
;       FILING DATE:  19-FEB-1992
;       APPLICATION NUMBER:  US 07/841,659
;       FILING DATE:  19-FEB-1992
;       APPLICATION NUMBER:  US 07/782,784
;       FILING DATE:  24-OCT-1991
;       APPLICATION NUMBER:  US 07/499,327
;       FILING DATE:  21-MAY-1990
;       APPLICATION NUMBER:  PCT/US88/03631
;       FILING DATE:  21-OCT-1988
;       APPLICATION NUMBER:  US 07/655,966
;       FILING DATE:  14-FEB-1991
;       APPLICATION NUMBER:  US 07/113,623
;       FILING DATE:  26-OCT-1987
;       APPLICATION NUMBER:  US 06/881,553
;       FILING DATE:  03-JUL-1986
;       APPLICATION NUMBER:  US 06/843,958
;       FILING DATE:  25-MAR-1986
;       APPLICATION NUMBER:  US 06/799,668
;       FILING DATE:  19-NOV-1985
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Foulke, Cynthia L.
;       REGISTRATION NUMBER:  32,364
;       REFERENCE/DOCKET NUMBER:  2409K7
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  908 298-2987
;       TELEFAX:  908-298-5388
;   INFORMATION FOR SEQ ID NO:  68:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-469-557-68

  Query Match             80.0%;  Score 16;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSSYW 8


RESULT 8
US-08-290-793B-68
; Sequence 68, Application US/08290793B
; Patent No. 5863537
;  GENERAL INFORMATION:
;     APPLICANT:  Dalie, Barbara
;     APPLICANT:  Le, Hung
;     APPLICANT:  Miller, Kenneth
;     APPLICANT:  Murgolo, Nicholas
;     APPLICANT:  Nguyen, Hanh
;     APPLICANT:  Tindall, Stephen
;     APPLICANT:  Zavodny, Paul
;     TITLE OF INVENTION:  Cloning and Expression of
;     TITLE OF INVENTION:  Humanized Monoclonal Antibodies
;     TITLE OF INVENTION:  Against Human Interleukin-4
;     NUMBER OF SEQUENCES:  69
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Schering-Plough Corporation
;       STREET:  2000 Galloping Hill Road
;       CITY:  Kenilworth
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07033-0530
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  Apple Macintosh
;       OPERATING SYSTEM:  Macintosh 6.0.5
;       SOFTWARE:  Microsoft Word 5.1A
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/290,793B
;       FILING DATE:  August 16, 1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/01301
;       FILING DATE:  19-FEB-1992
;       APPLICATION NUMBER:  US 07/841,659
;       FILING DATE:  19-FEB-1992
;       APPLICATION NUMBER:  US 07/782,784
;       FILING DATE:  24-OCT-1991
;       APPLICATION NUMBER:  US 07/499,327
;       FILING DATE:  21-MAY-1990
;       APPLICATION NUMBER:  PCT/US88/03631
;       FILING DATE:  21-OCT-1988
;       APPLICATION NUMBER:  US 07/655,966
;       FILING DATE:  14-FEB-1991
;       APPLICATION NUMBER:  US 07/113,623
;       FILING DATE:  26-OCT-1987
;       APPLICATION NUMBER:  US 06/881,553
;       FILING DATE:  03-JUL-1986
;       APPLICATION NUMBER:  US 06/843,958
;       FILING DATE:  25-MAR-1986
;       APPLICATION NUMBER:  US 06/799,668
;       FILING DATE:  19-NOV-1985
;     ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  Foulke, Cynthia L.
;       REGISTRATION NUMBER:  32,364
;       REFERENCE/DOCKET NUMBER:  2409K7
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  908 298-2987
;       TELEFAX:  908-298-5388
;   INFORMATION FOR SEQ ID NO:  68:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-290-793B-68

  Query Match             80.0%;  Score 16;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       4 FSSYW 8


RESULT 9
US-08-277-660A-16
; Sequence 16, Application US/08277660A
; Patent No. 5702908
;  GENERAL INFORMATION:
;    APPLICANT:  Picksley, Steven M.
;    APPLICANT:  Lane, David P.
;    TITLE OF INVENTION:  Interruption of Binding of MDM2 and P53
;    TITLE OF INVENTION:  Protein and Therapeutic Application Thereof
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,660A
;      FILING DATE:  20-JUL-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-60244/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-277-660A-16

  Query Match             80.0%;  Score 16;  DB 1;  Length 11;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       5 FSALW 9


RESULT 10
US-08-277-660A-17
; Sequence 17, Application US/08277660A
; Patent No. 5702908
;  GENERAL INFORMATION:
;    APPLICANT:  Picksley, Steven M.
;    APPLICANT:  Lane, David P.
;    TITLE OF INVENTION:  Interruption of Binding of MDM2 and P53
;    TITLE OF INVENTION:  Protein and Therapeutic Application Thereof
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/277,660A
;      FILING DATE:  20-JUL-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-60244/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-277-660A-17

  Query Match             80.0%;  Score 16;  DB 1;  Length 11;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       5 FSDAW 9


RESULT 11
US-08-424-957-29
; Sequence 29, Application US/08424957
; Patent No. 5770377
;  GENERAL INFORMATION:
;    APPLICANT:  Picksley, Steven M.
;    APPLICANT:  Lane, David P.
;    TITLE OF INVENTION:  Interruption of Binding of MDM2 and P53
;    TITLE OF INVENTION:  Protein and Therapeutic Application Thereof
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/424,957
;       FILING DATE:  19-APR-1995
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/277,660
;       FILING DATE:  20-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Dreger, Walter H.
;       REGISTRATION NUMBER:  24,190
;       REFERENCE/DOCKET NUMBER:  A-61228/WHD
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 781-1989
;       TELEFAX:  (415) 398-3249
;       TELEX:  910 277299
;   INFORMATION FOR SEQ ID NO:  29:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  unknown
US-08-424-957-29

  Query Match             80.0%;  Score 16;  DB 1;  Length 11;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       5 FSALW 9


RESULT 12
US-08-424-957-30
; Sequence 30, Application US/08424957
; Patent No. 5770377
;  GENERAL INFORMATION:
;    APPLICANT:  Picksley, Steven M.
;    APPLICANT:  Lane, David P.
;    TITLE OF INVENTION:  Interruption of Binding of MDM2 and P53
;    TITLE OF INVENTION:  Protein and Therapeutic Application Thereof
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/424,957
;      FILING DATE:  19-APR-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,660
;      FILING DATE:  20-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-61228/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
US-08-424-957-30

  Query Match             80.0%;  Score 16;  DB 1;  Length 11;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       5 FSDAW 9


RESULT 13
US-09-035-686-29
; Sequence 29, Application US/09035686
; Patent No. 6153391
;  GENERAL INFORMATION:
;    APPLICANT:  Picksley, Steven M.
;    APPLICANT:  Lane, David P.
;    TITLE OF INVENTION:  Interruption of Binding of MDM2 and P53
;    TITLE OF INVENTION:  Protein and Therapeutic Application Thereof
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/035,686
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/424,957
;      FILING DATE:  19-APR-1995
;      APPLICATION NUMBER:  US 08/277,660
;      FILING DATE:  20-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-61228/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
US-09-035-686-29

  Query Match             80.0%;  Score 16;  DB 4;  Length 11;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       5 FSALW 9


RESULT 14
US-09-035-686-30
; Sequence 30, Application US/09035686
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; Patent No. 6153391
;  GENERAL INFORMATION:
;    APPLICANT:  Picksley, Steven M.
;    APPLICANT:  Lane, David P.
;    TITLE OF INVENTION:  Interruption of Binding of MDM2 and P53
;    TITLE OF INVENTION:  Protein and Therapeutic Application Thereof
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/035,686
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/424,957
;      FILING DATE:  19-APR-1995
;      APPLICATION NUMBER:  US 08/277,660
;      FILING DATE:  20-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-61228/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
US-09-035-686-30

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  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
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Db       5 FSDAW 9


RESULT 15
US-08-406-330-32
; Sequence 32, Application US/08406330
; Patent No. 5817748
;  GENERAL INFORMATION:
;    APPLICANT:  Miller, Jonathan L.
;    APPLICANT:  Lyle, Vicki A.
;    TITLE OF INVENTION:  MIMOTOPES AND ANTI-MIMOTOPES OF
;    TITLE OF INVENTION:  HUMAN PLATELET GLYCOPROTEIN Ib/IX
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/406,330
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  20884/100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1636
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-406-330-32

  Query Match             80.0%;  Score 16;  DB 2;  Length 12;
  Best Local Similarity   40.0%;  Pred. No. 1.3e+03;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       3 FSSVW 7


Search completed: January 29, 2003, 14:18:21
Job time : 15 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:21:09 ; Search time 14 Seconds
(without alignments)
34.334 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11	55.0	5	2	A32516	cholecystokinin-5
2	11	55.0	5	2	A60803	neuropeptide - sea
3	11	55.0	5	2	JH0253	gut pentapeptide -
4	11	55.0	5	2	G37196	bradykinin-potenti
5	11	55.0	5	2	PT0281	Ig heavy chain CRD
6	11	55.0	5	2	PT0308	Ig heavy chain CRD
7	11	55.0	5	2	PT0729	T-cell receptor be
8	11	55.0	5	2	PT0580	T-cell receptor be
9	6	30.0	5	2	A44955	alkanal monooxygen
10	6	30.0	5	2	S70615	endo-1,4-beta-xyla
11	6	30.0	5	2	PS0324	ribulose-bisphosph
12	6	30.0	5	2	B45525	actin I - malaria
13	6	30.0	5	2	A44692	fulicin - giant Af
14	6	30.0	5	2	B61445	Leu-enkephalin - b
15	6	30.0	5	2	A61445	Met-enkephalin - b
16	6	30.0	5	2	JS0319	subesophageal gang
17	6	30.0	5	2	B61168	cocoonase (EC 3.4.
18	6	30.0	5	2	PT0278	Ig heavy chain CRD
19	6	30.0	5	2	PT0644	T-cell receptor be
20	6	30.0	5	4	A58728	serrawettin W2 - S
21	3	15.0	5	1	HOROHA	proctolin - Americ
22	3	15.0	5	2	B37325	pap fimbrial regul
23	3	15.0	5	2	I39964	ribosomal protein
24	3	15.0	5	2	I39966	ribosomal protein
25	3	15.0	5	2	I39965	ribosomal protein
26	3	15.0	5	2	I40469	dnaZX-like protein
27	3	15.0	5	2	E60274	major protein anti
28	3	15.0	5	2	F22565	R-phycoerythrin ga
29	3	15.0	5	2	PQ0009	angiotensin-conver
30	3	15.0	5	2	PQ0689	photosystem I 10.4
31	3	15.0	5	2	A60411	proctolin - Atlant
32	3	15.0	5	2	S68326	blood cell protein
33	3	15.0	5	3	JT0870	phytosulfokine alp
34	0	0.0	5	2	A60521	glycogen phosphory
35	0	0.0	5	2	JN0862	peptidyl-dipeptida
36	0	0.0	5	2	JN0860	peptidyl-dipeptida
37	0	0.0	5	2	C23751	spinal cord peptid
38	0	0.0	5	2	A26830	mitosis inhibiting
39	0	0.0	5	2	C41225	copper resistance
40	0	0.0	5	2	A41225	copper resistance
41	0	0.0	5	2	B41225	copper resistance
42	0	0.0	5	2	S70154	URF2 protein - Xan
3	0	0.0	5	2	I40702	primase - Citrobac
4	0	0.0	5	2	I40698	biotin B - Citroba
5	0	0.0	5	2	A32014	traM protein - Esc

Seq Length = 5 AA

ALIGNMENTS

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16
ecystokinin-5 - dog
ternate names: CCK-5
ecies: Canis lupus familiaris (dog)
te: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
cession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
A;Reference number: A32516; MUID:87153871; PMID:3826354
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <SHI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       5 W 5
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Db       2 W 2
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RESULT 2
A60803
neuropeptide - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60803
R;Graff, D.; Grimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A;Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemone
A;Reference number: A60803; MUID:88222764; PMID:2897223
A;Accession: A60803
A;Molecule type: protein
A;Residues: 1-5 <GRA>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       5 W 5
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Db       5 W 5
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RESULT 3
JH0253
gut pentapeptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253
R;Jesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
A;Accession: JH0253
A;Molecule type: protein
A;Residues: 1-5 <UES>
A;Experimental source: gut
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastr
, and of the circular muscle of the gastro-intestinal junction.

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 3 W 3

RESULT 4
G37196
bradykinin-potentiating peptide 7 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: G37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides f
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: G37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CIN>
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 3 W 3

RESULT 5
PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0281
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0281
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 4 W 4

RESULT 6
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0308
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0308
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 2 W 2

RESULT 7
PT0729
T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0640; PT0685; PT0729
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0640
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A;Accession: PT0685
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C
A;Accession: PT0729
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE3>
A;Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C;Keywords: T-cell receptor

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 5 W 5

RESULT 8
PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0580

R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0580
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 55.0%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 4 W 4

RESULT 9
A44955
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment
C;Species: Vibrio harveyi
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C;Accession: A44955
R;Paquatte, O.; Tu, S.C.
Photochem. Photobiol. 50, 817-825, 1989
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib
A;Reference number: A44955; MUID:90175700; PMID:2626493
A;Accession: A44955
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <PAQ>
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 30.0%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
|
Db 1 F 1

RESULT 10
S70615
endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (fragmen
N;Alternate names: xylanase
C;Species: Streptomyces sp.
A;Variety: Chainia sp. NCL 82.5.1
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C;Accession: S70615
R;Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.
Biochem. J. 316, 771-775, 1996
A;Title: Structural environment of an essential cysteine residue of xylanase from Chaini
A;Reference number: S70615; MUID:96265041; PMID:8670151
A;Accession: S70615
A;Molecule type: protein
A;Residues: 1-5 <RAO>
A;Experimental source: Chainia sp. strain NCL 82.5.1
A;Note: the source is designated as Chainia sp.
C;Function:
A;Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans
A;Pathway: fermentation of hemicellulose into ethanol
C;Keywords: glycosidase; hydrolase

Query Match 30.0%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
|
Db 3 F 3

RESULT 11
PS0324
ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998
C;Accession: PS0324
R;Tsugita, A.
submitted to JIPID, April 1993
A;Reference number: PS0206
A;Accession: PS0324
A;Molecule type: protein
A;Residues: 1-5 <TSU>
A;Experimental source: leaf, chlorophyll

Query Match 30.0%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
|
Db 1 F 1

RESULT 12
B45525
actin I - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Accession: B45525
R;Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoen
Mol. Biochem. Parasitol. 35, 167-176, 1989
A;Title: Stage-specific expression and genomic organization of the actin genes of the
A;Reference number: A45525; MUID:89364996; PMID:2671721
A;Accession: B45525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <WES>
A;Cross-references: GB:J03988
A;Note: the authors translated the codon GAA for residue 3 as Gly
C;Comment: The actin I gene contains no introns.

Query Match 30.0%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
|
Db 5 F 5

RESULT 13
A44692
fulicin - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C;Accession: A44692
R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.;
Biochem. Biophys. Res. Commun. 178, 486-493, 1991
A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated fro
A;Reference number: A44692; MUID:91315471; PMID:1859408
A;Accession: A44692
A;Molecule type: protein
A;Residues: 1-5 <OHT>
C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F;2/Modified site: D-asparagine (Asn) #status experimental
F;5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 30.0%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 F 1
           |
Db       1 F 1


RESULT 14
B61445
Leu-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: B61445
R;Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A;Reference number: A61445; MUID:84144823; PMID:6583690
A;Accession: B61445
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide

  Query Match             30.0%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 F 1
           |
Db       4 F 4


RESULT 15
A61445
Met-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: A61445
R;Leung, M.K.; Stefano, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A;Reference number: A61445; MUID:84144823; PMID:6583690
A;Accession: A61445
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide

  Query Match             30.0%;  Score 6;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 F 1
           |
Db       4 F 4


Search completed: January 29, 2003, 14:23:17
Job time : 14 secs
```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:18:23 ; Search time 11 Seconds
(without alignments)
18.853 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11	55.0	5	1	BPP7_BOTIN	P30425 bothrops in
2	11	55.0	5	1	UF01_MOUSE	P38639 mus musculu
3	6	30.0	5	1	AL14_CARMA	P81817 carcinus ma
4	6	30.0	5	1	EI03_LITRU	P82099 litoria rub
5	6	30.0	5	1	EI04_LITRU	P82100 litoria rub
6	6	30.0	5	1	FARP_ARTTR	P41853 artioposthi
7	6	30.0	5	1	PAP2_PARMA	P81864 pardachirus
8	6	30.0	5	1	RE11_LITRU	P82070 litoria rub
9	6	30.0	5	1	RE21_LITRU	P82071 litoria rub
10	6	30.0	5	1	RE31_LITRU	P82072 litoria rub
11	6	30.0	5	1	RE32_LITRU	P82073 litoria rub
12	6	30.0	5	1	SUGA_ACHDO	P19991 acheta dome
13	6	30.0	5	1	TPIS_CANFA	P54714 canis famil
14	6	30.0	5	1	UC22_MAIZE	P80628 zea mays (m
15	3	15.0	5	1	PRCT_PERAM	P01373 periplaneta
16	3	15.0	5	1	PSK_DAUCA	P58261 daucus caro
17	0	0.0	5	1	BIOA_CITFR	P13071 citrobacter
18	0	0.0	5	1	BIOB_CITFR	P12997 citrobacter
19	0	0.0	5	1	TRM3_ECOLI	P13973 escherichia
20	0	0.0	5	1	UXA4_CHLTR	P38005 chlamydia t

ALIGNMENTS

RESULT 1
BPP7_BOTIN
ID BPP7_BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR; G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 3 W 3

RESULT 2
UF01_MOUSE
ID UF01_MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 55.0%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 3
AL14_CARMA
ID AL14_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

```
DE   Carcinustatin 14.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC   Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC   Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC   -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       5       5       AMIDATION (POTENTIAL).
SQ   SEQUENCE   5 AA;  586 MW;  672879D5AB300000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 F 1
          |
Db      3 F 3


RESULT 4
EI03_LITRU
ID   EI03_LITRU     STANDARD;      PRT;     5 AA.
AC   P82099;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Electrin 3.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:639-645(1999).
CC   -!- SUBCELLULAR LOCATION: SECRETED.
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  630 MW;  668761F2C9A00000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 F 1
          |
Db      1 F 1


RESULT 5
EI04_LITRU
ID   EI04_LITRU     STANDARD;      PRT;     5 AA.
AC   P82100;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Electrin 4.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:639-645(1999).
CC   -!- SUBCELLULAR LOCATION: SECRETED.
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  616 MW;  61F2D1A059A00000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 F 1
          |
Db      1 F 1


RESULT 6
FARP_ARTTR
ID   FARP_ARTTR     STANDARD;      PRT;     5 AA.
AC   P41853;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   FMRFamide-like neuropeptide RYIRF-amide.
OS   Artioposthia triangulata.
OC   Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC   Terricola; Geoplanidae; Arthurdendyus.
OX   NCBI_TaxID=132421;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RX   MEDLINE=94211927; PubMed=7909164;
RA   Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
RT   "RYIRFamide: a turbellarian FMRFamide-related peptide (FaRP).";
RL   Regul. Pept. 50:37-43(1994).
CC   -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC       FAMILY.
KW   Neuropeptide; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  754 MW;  69D4004B44600000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 F 1
          |
Db      5 F 5


RESULT 7
PAP2_PARMA
ID   PAP2_PARMA     STANDARD;      PRT;     5 AA.
AC   P81864;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Pardaxin II (PXII) (Fragment).
OS   Pardachirus marmoratus (Red sea moses sole).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Soleoidei; Soleidae; Pardachirus.
```

```
OX   NCBI_TaxID=31087;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=87057369; PubMed=3782138;
RA   Lazarovici P., Primor N., Loew L.M.;
RT   "Purification and pore-forming activity of two hydrophobic
RT   polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT   marmoratus).";
RL   J. Biol. Chem. 261:16704-16713(1986).
CC   -!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC       PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
CC       IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC   -!- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW   Toxin.
FT   NON_TER       5       5
SQ   SEQUENCE   5 AA;  614 MW;  7769C9C9C8100000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 F 1
          |
Db      2 F 2


RESULT 8
RE11_LITRU
ID   RE11_LITRU     STANDARD;      PRT;     5 AA.
AC   P82070;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 1.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  598 MW;  6DD9C9CAB2A00000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 F 1
          |
Db      3 F 3


RESULT 9
RE21_LITRU
ID   RE21_LITRU     STANDARD;      PRT;     5 AA.
AC   P82071;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 2.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  626 MW;  6DD9C9CB10300000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 F 1
          |
Db      3 F 3


RESULT 10
RE31_LITRU
ID   RE31_LITRU     STANDARD;      PRT;     5 AA.
AC   P82072;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 3.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. the skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC   -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW   Amphibian skin; Amidation.
FT   MOD_RES       5       5       AMIDATION.
SQ   SEQUENCE   5 AA;  656 MW;  71A9C9CB10300000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 F 1
          |
Db      3 F 3


RESULT 11
RE32_LITRU
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```
ID   RE32_LITRU     STANDARD;      PRT;     5 AA.
AC   P82073;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Rubellidin 3.2.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:639-645(1999).
CC   -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC       ACTIVITY.
CC   -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW   Amphibian skin.
SQ   SEQUENCE   5 AA;  570 MW;  71A9C9C862A00000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 F 1
           |
Db       3 F 3


RESULT 12
SUGA_ACHDO
ID   SUGA_ACHDO     STANDARD;      PRT;     5 AA.
AC   P19991;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Suboesophageal ganglion pentapeptide.
OS   Acheta domesticus (House cricket).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;
OC   Gryllidae; Gryllinae; Acheta.
OX   NCBI_TaxID=6997;
RN   [1]
RP   SEQUENCE.
RA   Wicker C., Wicker C.;
RT   "Isolation and structure of a peptide isolated from the
RT   suboesophageal ganglion of Acheta domesticus (orthoptera).";
RL   Comp. Biochem. Physiol. 88C:185-187(1987).
CC   -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBOESOPHAGEAL
CC       GANGLIA.
DR   PIR; JS0319; JS0319.
SQ   SEQUENCE   5 AA;  476 MW;  69D76DDDDDB00000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 F 1
           |
Db       5 F 5


RESULT 13
TPIS_CANFA
ID   TPIS_CANFA     STANDARD;      PRT;     5 AA.
AC   P54714;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
GN   TPI1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=98163340; PubMed=9504812;
RA   Dunn M.J., Corbett J.M., Wheeler C.H.;
RT   "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT   dog heart proteins.";
RL   Electrophoresis 18:2795-2802(1997).
CC   -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC       phosphate.
CC   -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR   HSC-2DPAGE; P54714; DOG.
DR   InterPro; IPR000652; Triophos_ismrse.
DR   PROSITE; PS00171; TIM; PARTIAL.
KW   Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW   Pentose shunt.
FT   NON_TER       1      1
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  550 MW;  64444862C9A00000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 F 1
           |
Db       1 F 1


RESULT 14
UC22_MAIZE
ID   UC22_MAIZE     STANDARD;      PRT;     5 AA.
AC   P80628;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
DE   (Fragment).
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Coleoptile;
RA   Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA   Pernollet J.-C., Zivy M., de Vienne D.;
RT   "The maize two dimensional gel protein database: towards an integrated
RT   genome analysis program.";
RL   Theor. Appl. Genet. 93:997-1005(1996).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
DR   Maize-2DPAGE; P80628; COLEOPTILE.
DR   MaizeDB; 123954; -.
FT   NON_TER       1      1
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  654 MW;  72CB19C9C0300000 CRC64;

  Query Match             30.0%;  Score 6;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 F 1
```

```
Db      2 F 2


RESULT 15
PRCT_PERAM
ID   PRCT_PERAM     STANDARD;      PRT;     5 AA.
AC   P01373;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Proctolin.
OS   Periplaneta americana (American cockroach),
OS   Limulus polyphemus (Atlantic horseshoe crab), and
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC   Blattoidea; Blattidae; Periplaneta.
OX   NCBI_TaxID=6978, 6850, 6759;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=P.americana;
RX   MEDLINE=76074708; PubMed=576;
RA   Starratt A.N., Brown B.E.;
RT   "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT   in insects.";
RL   Life Sci. 17:1253-1256(1975).
RN   [2]
RP   BIOLOGICAL SOURCE.
RC   SPECIES=P.americana;
RX   MEDLINE=81225865; PubMed=6113690;
RA   O'Shea M., Adams M.E.;
RT   "Pentapeptide (proctolin) associated with an identified neuron.";
RL   Science 213:567-569(1981).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=L.polyphemus;
RX   MEDLINE=90287800; PubMed=2356151;
RA   Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA   Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA   Shabanowitz J.;
RT   "Identification of proctolin in the central nervous system of the
RT   horseshoe crab, Limulus polyphemus.";
RL   Peptides 11:205-211(1990).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=C.maenas;
RX   MEDLINE=86232789; PubMed=2872661;
RA   Stangier J., Dircksen H., Keller R.;
RT   "Identification and immunocytochemical localization of proctolin in
RT   pericardial organs of the shore crab, Carcinus maenas.";
RL   Peptides 7:67-72(1986).
CC   -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC       MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC   -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC       THE CRAB PERICARDIAL ORGANS.
DR   PIR; A01644; HOROHA.
DR   PIR; A60411; A60411.
KW   Neuropeptide.
SQ   SEQUENCE   5 AA;  649 MW;  71B7673B44600000 CRC64;

  Query Match             15.0%;  Score 3;  DB 1;  Length 5;
  Best Local Similarity   0.0%;  Pred. No. 1.1e+05;
  Matches    0;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 F 1
          :
Db      2 Y 2


Search completed: January 29, 2003, 14:22:21
Job time : 12 secs
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:20:44 ; Search time 28 Seconds
(without alignments)
36.794 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6	30.0	5	13	P83308	P83308 gallus gall
2	0	0.0	5	2	P83073	P83073 bacillus ce
3	0	0.0	5	10	Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1
P83308
ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE FMRFamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=BRAIN;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRFamide.";
RL Nature 305:328-330(1983).
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 30.0%; Score 6; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
|
Db 5 F 5

RESULT 2
P83073
ID P83073 PRELIMINARY; PRT; 5 AA.
AC P83073;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE 88 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 6.7e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 F 1

Db 1 M 1

RESULT 3
Q99007
ID Q99007 PRELIMINARY; PRT; 5 AA.
AC Q99007;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1) (Fragment).
GN AMY1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.

```
RC   STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX   MEDLINE=91329704; PubMed=1831055;
RA   Jacobsen J.V., Close T.J.;
RT   "Control of transient expression of chimaeric genes by gibberellic
RT   acid and abscisic acid in protoplasts prepared from mature barley
RT   aleurone layers.";
RL   Plant Mol. Biol. 16:713-721(1991).
CC   -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC       LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
CC   -!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC   -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC       BARLEY.
DR   EMBL; X54643; CAA38455.1; -.
KW   Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW   Calcium; Multigene family.
FT   NON_TER       5      5
SQ   SEQUENCE   5 AA;  600 MW;  61E3344DD6F00000 CRC64;

  Query Match             0.0%;  Score 0;  DB 10;  Length 5;
  Best Local Similarity   0.0%;  Pred. No. 6.7e+05;
  Matches    0;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 F 1

Db       1 M 1


Search completed: January 29, 2003, 14:22:55
Job time : 28 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:18:03 ; Search time 34 Seconds
(without alignments)
19.596 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 13629

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15	75.0	5	17	AAW17807	Cyclic pentapeptid
2	15	75.0	5	17	AAW17812	Cyclic pentapeptid
3	15	75.0	5	17	AAW17806	Cyclic pentapeptid
4	15	75.0	5	20	AAY33038	Carbohydrate antig
5	15	75.0	5	21	AAB07280	Motif binding to a
6	14	70.0	5	13	AAR26471	Serotinin release
7	14	70.0	5	13	AAR26473	Serotinin release
8	14	70.0	5	13	AAR29438	Endothelin antagon
9	14	70.0	5	13	AAR29448	Endothelin antagon
10	14	70.0	5	15	AAR47436	Cyclic peptide whi
11	14	70.0	5	15	AAR69220	Endothelin C-termi
12	14	70.0	5	15	AAR69260	Endothelin C-termi
13	14	70.0	5	15	AAR69210	Endothelin C-termi
14	14	70.0	5	16	AAR89837	Melanotrophic rele
15	14	70.0	5	16	AAR89842	Melanotrophic rele
16	14	70.0	5	17	AAW17808	Cyclic pentapeptid
17	14	70.0	5	17	AAW17809	Cyclic pentapeptid
18	14	70.0	5	17	AAR89911	p53/MDM2 binding i
19	14	70.0	5	17	AAR89912	p53/MDM2 binding i
20	14	70.0	5	18	AAW22914	Low density lipopr
21	14	70.0	5	19	AAW78939	Antidepressant MIF
22	14	70.0	5	19	AAW78938	Antidepressant MIF
23	14	70.0	5	19	AAW50861	Cyclic peptide whi
24	14	70.0	5	20	AAY14091	Affinity ligand fo
25	14	70.0	5	20	AAY17477	Antidepressant age
26	14	70.0	5	21	AAY58280	Human p53 consensu
27	14	70.0	5	23	AAO20822	Hydrophobic intera
28	13	65.0	5	6	AAP50708	Hexapeptide somato
29	13	65.0	5	16	AAR89838	Melanotrophic rele
30	13	65.0	5	16	AAR89840	Melanotrophic rele
31	13	65.0	5	16	AAR89841	Melanotrophic rele
32	13	65.0	5	16	AAR89843	Melanotrophic rele
33	13	65.0	5	16	AAR89828	Melanotrophic rele
34	13	65.0	5	16	AAR89829	Melanotrophic rele
35	13	65.0	5	16	AAR89830	Melanotrophic rele
36	13	65.0	5	16	AAR89831	Melanotrophic rele
37	13	65.0	5	16	AAR89832	Melanotrophic rele
38	13	65.0	5	16	AAR89833	Melanotrophic rele
39	13	65.0	5	16	AAR89834	Melanotrophic rele
40	13	65.0	5	16	AAR89835	Melanotrophic rele
41	13	65.0	5	16	AAR89836	Melanotrophic rele
42	13	65.0	5	16	AAR89839	Melanotrophic rele
43	13	65.0	5	16	AAR89818	Melanotrophic rele
44	13	65.0	5	16	AAR89820	Melanotrophic rele
45	13	65.0	5	16	AAR89821	Melanotrophic rele

ALIGNMENTS

RESULT 1
AAW17807
ID AAW17807 standard; peptide; 5 AA.
XX
AC AAW17807;
XX
DT 07-JUL-1997 (first entry)
XX
DE Cyclic pentapeptide #23 used in LH-RH receptor antagonist.
XX
KW Luteinising hormone releasing hormone receptor; LH-RH; antagonist;
KW sex-hormone; human; veterinary medicine; cancer; prostate; uterus;
KW breast; pituitary; prostatomegaly; endometriosis; hysteromyoma;
KW precocious puberty; amenorrhoea; premenstrual syndrome; cyclic;
KW multilocular ovarian syndrome; comedo; pregnancy; contraception;
KW ovulation; menstrual cycle; oestrus; meat quality; growth; spawning;
KW fish; testosterone; superagonist; leuprorelin acetate.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Joined via a peptide linkage to Trp5"
FT Modified-site 2
FT /note= "Opt. N-pToluenesulphonylarginine, D-form
FT residue"
FT Modified-site 3
FT /label= Nal
FT Misc-difference 4
FT /note= "D-form residue"
FT Modified-site 5
FT /note= "Joined via a peptide linkage to Phe1"
XX
OS Synthetic.
XX

```
PN   WO9634012-A1.
XX
PD   31-OCT-1996.
XX
PF   25-APR-1996;   96WO-JP01140.
XX
PR   09-MAY-1995;   95JP-0110933.
PR   28-APR-1995;   95JP-0106775.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Furuya S,  Kato K,  Kitada C;
XX
DR   WPI; 1996-497569/49.
XX
PT   Cyclic penta:peptide(s), some new, as LH-RH receptor antagonists -
PT   used to treat or prevent sex hormone dependent disorders, e.g.
PT   cancer, also for control of pregnancy and menstruation and to
PT   improve meat quality in animals
XX
PS   Example 40-41; Page 170; 198pp; English.
XX
CC   This peptide represents a cyclic peptide which is included in the
CC   luteinising hormone releasing hormone (LH-RH) receptor antagonist
CC   composition of the invention. Peptides such as this are used to
CC   prevent or treat sex-hormone dependent disorders in human or veterinary
CC   medicine, esp. cancers (of the prostate, uterus, breast or pituitary),
CC   prostatomegaly, endometriosis, hysteromyoma or precocious puberty, but
CC   also amenorrhoea, premenstrual syndrome, multilocular ovarian syndrome,
CC   comedo, etc.; also to control pregnancy (contraception for men or women,
CC   also to induce ovulation) and the menstrual cycle.  They are also used
CC   to control oestrus in animals, to improve meat quality and control
CC   growth, and to promote spawning in fish.  They may also inhibit the
CC   transient increase in testosterone blood levels caused by admin. of
CC   superagonists such as leuprorelin acetate.
XX
SQ   Sequence   5 AA;

  Query Match             75.0%;  Score 15;  DB 17;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 7.7e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          | | |
Db      1 FRXAW 5


RESULT 2
AAW17812
ID   AAW17812 standard; peptide; 5 AA.
XX
AC   AAW17812;
XX
DT   07-JUL-1997  (first entry)
XX
DE   Cyclic pentapeptide #28 used in LH-RH receptor antagonist.
XX
KW   Luteinising hormone releasing hormone receptor; LH-RH; antagonist;
KW   sex-hormone; human; veterinary medicine; cancer; prostate; uterus;
KW   breast; pituitary; prostatomegaly; endometriosis; hysteromyoma;
KW   precocious puberty; amenorrhoea; premenstrual syndrome; cyclic;
KW   multilocular ovarian syndrome; comedo; pregnancy; contraception;
KW   ovulation; menstrual cycle; oestrus; meat quality; growth; spawning;
KW   fish; testosterone; superagonist; leuprorelin acetate.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Joined via a peptide linkage to Trp5"
FT   Modified-site   2
FT                   /note= "N-pToluenesulphonylarginine, D-form residue"
FT   Modified-site   3
FT                   /label= OTHER
FT                   /note= "Parafluorophenylalanine"
FT   Misc-difference 4
FT                   /note= "D-form residue"
FT   Modified-site   5
FT                   /note= "Joined via a peptide linkage to Phe1"
XX
OS   Synthetic.
XX
PN   WO9634012-A1.
XX
PD   31-OCT-1996.
XX
PF   25-APR-1996;   96WO-JP01140.
XX
PR   09-MAY-1995;   95JP-0110933.
PR   28-APR-1995;   95JP-0106775.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Furuya S,  Kato K,  Kitada C;
XX
DR   WPI; 1996-497569/49.
XX
PT   Cyclic penta:peptide(s), some new, as LH-RH receptor antagonists -
PT   used to treat or prevent sex hormone dependent disorders, e.g.
PT   cancer, also for control of pregnancy and menstruation and to
PT   improve meat quality in animals
XX
PS   Example 50; Page 176; 198pp; English.
XX
CC   This peptide represents a cyclic peptide which is included in the
CC   luteinising hormone releasing hormone (LH-RH) receptor antagonist
CC   composition of the invention. Peptides such as this are used to
CC   prevent or treat sex-hormone dependent disorders in human or veterinary
CC   medicine, esp. cancers (of the prostate, uterus, breast or pituitary),
CC   prostatomegaly, endometriosis, hysteromyoma or precocious puberty, but
CC   also amenorrhoea, premenstrual syndrome, multilocular ovarian syndrome,
CC   comedo, etc.; also to control pregnancy (contraception for men or women,
CC   also to induce ovulation) and the menstrual cycle.  They are also used
CC   to control oestrus in animals, to improve meat quality and control
CC   growth, and to promote spawning in fish.  They may also inhibit the
CC   transient increase in testosterone blood levels caused by admin. of
CC   superagonists such as leuprorelin acetate.
XX
SQ   Sequence   5 AA;

  Query Match             75.0%;  Score 15;  DB 17;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 7.7e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          | | |
Db      1 FRXAW 5


RESULT 3
AAW17806
ID   AAW17806 standard; peptide; 5 AA.
XX
AC   AAW17806;
XX
DT   07-JUL-1997  (first entry)
XX
DE   Cyclic pentapeptide #22 used in LH-RH receptor antagonist.
XX
KW   Luteinising hormone releasing hormone receptor; LH-RH; antagonist;
KW   sex-hormone; human; veterinary medicine; cancer; prostate; uterus;
KW   breast; pituitary; prostatomegaly; endometriosis; hysteromyoma;
KW   precocious puberty; amenorrhoea; premenstrual syndrome; cyclic;
KW   multilocular ovarian syndrome; comedo; pregnancy; contraception;
KW   ovulation; menstrual cycle; oestrus; meat quality; growth; spawning;
KW   fish; testosterone; superagonist; leuprorelin acetate.
XX
FH   Key             Location/Qualifiers
```

```
FT   Modified-site   1
FT                   /note= "Joined via a peptide linkage to Trp5, opt.
FT                          parachlorophenylalanine"
FT   Misc-difference 2
FT                   /note= "opt. N-(4-methoxy-2,3,6-trimethylbenzene-
FT                          sulphonyl)arginine, Arg, N-pToluenesulphonyl-
FT                          arginine, opt. D-form residue"
FT   Modified-site   3
FT                   note= "opt. parachlorophenylalanine"
FT   Misc-difference 4
FT                   /note= "D-form residue"
FT   Modified-site   5
FT                   /note= "Joined via a peptide linkage to Phe1"
XX
OS   Synthetic.
XX
PN   WO9634012-A1.
XX
PD   31-OCT-1996.
XX
PF   25-APR-1996;   96WO-JP01140.
XX
PR   09-MAY-1995;   95JP-0110933.
PR   28-APR-1995;   95JP-0106775.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Furuya S,  Kato K,  Kitada C;
XX
DR   WPI; 1996-497569/49.
XX
PT   Cyclic penta:peptide(s), some new, as LH-RH receptor antagonists -
PT   used to treat or prevent sex hormone dependent disorders, e.g.
PT   cancer, also for control of pregnancy and menstruation and to
PT   improve meat quality in animals
XX
PS   Example 33-39, 42-43 and 47; Page 167; 198pp; English.
XX
CC   This peptide represents a cyclic peptide which is included in the
CC   luteinising hormone releasing hormone (LH-RH) receptor antagonist
CC   composition of the invention. Peptides such as this are used to
CC   prevent or treat sex-hormone dependent disorders in human or veterinary
CC   medicine, esp. cancers (of the prostate, uterus, breast or pituitary),
CC   prostatomegaly, endometriosis, hysteromyoma or precocious puberty, but
CC   also amenorrhoea, premenstrual syndrome, multilocular ovarian syndrome,
CC   comedo, etc.; also to control pregnancy (contraception for men or women,
CC   also to induce ovulation) and the menstrual cycle.  They are also used
CC   to control oestrus in animals, to improve meat quality and control
CC   growth, and to promote spawning in fish.  They may also inhibit the
CC   transient increase in testosterone blood levels caused by admin. of
CC   superagonists such as leuprorelin acetate.
XX
SQ   Sequence   5 AA;

  Query Match             75.0%;  Score 15;  DB 17;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 7.7e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FRFAW 5


RESULT 4
AAY33038
ID   AAY33038 standard; peptide; 5 AA.
XX
AC   AAY33038;
XX
DT   03-NOV-1999  (first entry)
XX
DE   Carbohydrate antigen peptide mimotope 11.
XX
KW   Mimotope; antigen; carbohydrate; antibody; mimic; vaccine; adjuvant;
KW   tumour immunity; cancer therapy; antibacterial; immune response;
KW   immunogenicity; anti-idiotype; T cell response manipulation.
XX
OS   Synthetic.
XX
PN   WO9940433-A1.
XX
PD   12-AUG-1999.
XX
PF   04-FEB-1999;   99WO-US02405.
XX
PR   04-FEB-1998;   98US-0073690.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Kieber-Emmons T;
XX
DR   WPI; 1999-527317/44.
XX
PT   Peptides and recombinant antibody mimics of carbohydrate antigens,
PT   used for, e.g. treatment of cancer and infection
XX
PS   Claim 21; Page 72; 88pp; English.
XX
CC   This invention describes a novel method for preparing a peptide or
CC   recombinant antibody, which mimics an antigenic carbohydrate. The
CC   peptides and recombinant antibodies prepared to mimic antigenic
CC   carbohydrates can be used to enhance binding of anti-antigenic
CC   carbohydrate antibodies to the antigenic carbohydrate, e.g. as vaccine
CC   adjuvants. The peptides can be used to inhibit binding of a ligand to a
CC   receptor, which is an antigenic carbohydrate. The methods are used to
CC   prepare the peptides and antigenic antibodies, which mimic the antigenic
CC   carbohydrates. Carbohydrate-conjugate vaccines could be used in tumour
CC   immunity and cancer therapy. The peptides and antibodies can also be
CC   used as antibacterials. Peptides that mimic carbohydrate antigens can be
CC   formulated to develop a longer lasting immune response. Other advantages
CC   of the peptide mimics are; (1) the chemical composition and purity of
CC   synthesized peptides can be precisely defined; (2) the immunogenicity
CC   of the peptides can be significantly enhanced by polymerization or
CC   addition or relatively small carrier molecules that reduce the total
CC   amount of antigen required for immunization; (3) peptide synthesis may
CC   be more practical than synthesis of carbohydrate-protein conjugates or
CC   the production of anti-idiotypes; (4) peptide mimicking sequences can
CC   be engineered into DNA plasmids for DNA vaccination to further
CC   manipulate T cell responses. AAY33028-Y33087 represent the carbohydrate
CC   antigen peptide mimotopes described in the invention.
XX
SQ   Sequence   5 AA;

  Query Match             75.0%;  Score 15;  DB 20;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 7.7e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FSLLW 5


RESULT 5
AAB07280
ID   AAB07280 standard; peptide; 5 AA.
XX
AC   AAB07280;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Motif binding to anti-Lewis antigen anibody BR55-2.
XX
KW   Human; peptido-mimetic; tumour metastasis; E-selectin;
KW   adhesion molecule; Lewis antigen; anti-adhesion therapy.
XX
OS   Unidentified.
```

XX
PN WO200027420-A1.
XX
PD 18-MAY-2000.
XX
PF 05-NOV-1999; 99WO-US26277.
XX
PR 06-NOV-1998; 98US-0107478.
XX
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Blaszczyk-Thurin M, Kieber-Emmons T;
XX
DR WPI; 2000-376309/32.
XX
PT Peptidomimetics of carbohydrate Lewis ligands useful for modulating
PT inflammation, metastasis and angiogenesis -
XX
PS Example 5; Page 37; 107pp; English.
XX
CC Tumour metastasis requires detachment of malignant cells from the primary
CC tumour, penetration of blood or lymph vessels and attachment to the
CC endothelium of distant organs, ultimately resulting in the formation of
CC new tumours. The selectin family of adhesion molecules is implicated in
CC this process. E-selectin is a calcium-dependent molecule expressed by
CC activated vascular endothelium. E-selectins bind to glycoconjugates
CC carrying a terminal tetrasaccharide Lewis antigen, which are found on
CC tumour cell surfaces. One such Lewis antigen is Lewis Y (LeY). The
CC binding of selectin molecules to their ligands is thought to be an
CC important step in metastasis. Therefore, inhibition of
CC E-selectin-dependent carbohydrate-mediated interactions is thought to
CC be a target for anti-cancer therapy. The present sequence is a non
CC planar-X-planar type motif. This motif is thought to bind to anti-LeY
CC antibody BR55-2. BR55-2 is a peptido-mimetics of E-selectins. Peptides
CC that block E-selectin-LeY binding and therefore adhesion of tumour cells
CC and leukocytes to endothelial cells inhibit metastasis.
XX
SQ Sequence 5 AA;

Query Match 75.0%; Score 15; DB 21; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 1 FSLLW 5

RESULT 6
AAR26471
ID AAR26471 standard; peptide; 5 AA.
XX
AC AAR26471;
XX
DT 22-OCT-1992 (first entry)
XX
DE Serotinin release inhibitor peptide.
XX
KW Ganglion; konaganishi; tortoise roll shell; nervous; muscular;
KW system; neurotransmitter; psychotropic; circulatory; drug.
XX
OS Tortoise roll shell.
XX
PN JP04091096-A.
XX
PD 24-MAR-1992.
XX
PF 02-APR-1990; 90JP-0087827.
XX
PR 02-APR-1990; 90JP-0087827.
XX
PA (SUNR) SUNTORY LTD.
XX
DR WPI; 1992-148003/18.
XX
PT New glycyl-tryprophan and oligopeptide(s) contg. it - esp.
PT alanyl-prolyl deriv., as serotonin release inhibitor for
PT psychotropic and circulatory agent,and control of mono:amine or
PT peptide neuro-transmitter
XX
PS Claim 1; Page 1; 10pp; Japanese.
XX
CC The peptide (or forms of it truncated from the N-terminus) was prepd.
CC by extraction from ganglion of konaganishi (tortoise roll shell)
CC with organic solvent, adsorption chromatography and gel filtration.
CC The oligopeptide is a useful reagent in biology or medical science
CC relating to the physiology of the nervous muscular system. It can
CC also be used for controlling monoamine or peptide neurotransmitter
CC relating reactions (e.g. inhibiting serotonin release) and as a
CC psychotropic or circulatory drug.
CC See also AAR26472-3.
XX
SQ Sequence 5 AA;

Query Match 70.0%; Score 14; DB 13; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
| |
Db 1 FAPGW 5

RESULT 7
AAR26473
ID AAR26473 standard; peptide; 5 AA.
XX
AC AAR26473;
XX
DT 22-OCT-1992 (first entry)
XX
DE Serotinin release inhibitor peptide.
XX
KW Ganglion; konaganishi; tortoise roll shell; nervous; muscular;
KW system; neurotransmitter; psychotropic; circulatory; drug.
XX
OS Tortoise roll shell.
XX
PN JP04091096-A.
XX
PD 24-MAR-1992.
XX
PF 02-APR-1990; 90JP-0087827.
XX
PR 02-APR-1990; 90JP-0087827.
XX
PA (SUNR) SUNTORY LTD.
XX
DR WPI; 1992-148003/18.
XX
PT New glycyl-tryprophan and oligopeptide(s) contg. it - esp.
PT alanyl-prolyl deriv., as serotonin release inhibitor for
PT psychotropic and circulatory agent,and control of mono:amine or
PT peptide neuro-transmitter
XX
PS Claim 1; Page 1; 10pp; Japanese.
XX
CC The peptide (or forms of it truncated from the N-terminus) was prepd.
CC by extraction from ganglion of konaganishi (tortoise roll shell)
CC with organic solvent, adsorption chromatography and gel filtration.
CC The oligopeptide is a useful reagent in biology or medical science
CC relating to the physiology of the nervous muscular system. It can
CC also be used for controlling monoamine or peptide neurotransmitter
CC relating reactions (e.g. inhibiting serotonin release) and as a
CC psychotropic or circulatory drug.

```
CC   See also AAR26471-3.
XX
SQ   Sequence   5 AA;

  Query Match             70.0%;  Score 14;  DB 13;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 7.7e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FSPGW 5


RESULT 8
AAR29438
ID   AAR29438 standard; peptide; 5 AA.
XX
AC   AAR29438;
XX
DT   13-APR-1993  (first entry)
XX
DE   Endothelin antagonist peptide.
XX
KW   Hypertension; myocardial infarction; congestive heart failure;
KW   endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
KW   acute renal failure; preeclampsia; diabetes; metabolic;
KW   endocrinological; neurological; disorders.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "(Ac- or 1-adamantyl acetic acid)- D-Phe"
XX
PN   WO9220706-A.
XX
PD   26-NOV-1992.
XX
PF   24-APR-1992;   92WO-US03408.
XX
PR   16-MAY-1991;   91US-0701274.
PR   18-DEC-1991;   91US-0809746.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Cody WL,  Depue P,  Doherty AM,  Taylor MD;
XX
DR   WPI; 1992-415706/50.
XX
PT   New peptide(s) used as endothelin antagonists - for treating
PT   hypertension, metabolic and endocrine disorders, heart failure,
PT   diabetes, asthma, neurological disorders, etc.
XX
PS   Claim 5; Page 94; 116pp; English.
XX
CC   The peptide is an endothelin antagonist useful in controlling
CC   hypertension, myocardial infarction, congestive heart failure,
CC   endotoxic shock, subarachnoid haemorrhage, asthma, arrhythmias,
CC   acute renal failure, preeclampsia, diabetes and metabolic,
CC   endocrinological and neurological disorders. Administration is oral
CC   parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/
CC   day. It may be prepared by conventional peptide synthesis.
XX
SQ   Sequence   5 AA;

  Query Match             70.0%;  Score 14;  DB 13;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 7.7e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FDIIW 5


RESULT 9
AAR29448
ID   AAR29448 standard; peptide; 5 AA.
XX
AC   AAR29448;
XX
DT   13-APR-1993  (first entry)
XX
DE   Endothelin antagonist peptide.
XX
KW   Hypertension; myocardial infarction; congestive heart failure;
KW   endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
KW   acute renal failure; preeclampsia; diabetes; metabolic;
KW   endocrinological; neurological; disorders.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "Ac-D-Phe"
XX
PN   WO9220706-A.
XX
PD   26-NOV-1992.
XX
PF   24-APR-1992;   92WO-US03408.
XX
PR   16-MAY-1991;   91US-0701274.
PR   18-DEC-1991;   91US-0809746.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Cody WL,  Depue P,  Doherty AM,  Taylor MD;
XX
DR   WPI; 1992-415706/50.
XX
PT   New peptide(s) used as endothelin antagonists - for treating
PT   hypertension, metabolic and endocrine disorders, heart failure,
PT   diabetes, asthma, neurological disorders, etc.
XX
PS   Claim 5; Page 95; 116pp; English.
XX
CC   The peptide is an endothelin antagonist useful in controlling
CC   hypertension, myocardial infarction, congestive heart failure,
CC   endotoxic shock, subarachnoid haemorrhage, asthma, arrhythmias,
CC   acute renal failure, preeclampsia, diabetes and metabolic,
CC   endocrinological and neurological disorders. Administration is oral
CC   parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/
CC   day. It may be prepared by conventional peptide synthesis.
XX
SQ   Sequence   5 AA;

  Query Match             70.0%;  Score 14;  DB 13;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 7.7e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FLDIW 5


RESULT 10
AAR47436
ID   AAR47436 standard; peptide; 5 AA.
XX
AC   AAR47436;
XX
DT   30-JUN-1994  (first entry)
XX
DE   Cyclic peptide which modulates endothelin activity.
XX
KW   Cyclic; peptide; endothelin; inhibitor; receptor; detection;
```

```
KW   isolation; antagonist; hypertension; pulmonary hypertension;
KW   cardiovascular disease; bronchoconstriction; asthma;
KW   inflammatory disease; ophthalmolgic shock; anaphylactic shock;
KW   haemorrhagic shock; gastroenteric disease; renal failure;
KW   endotoxin shock; menstrual disorders; obstretic conditions;
KW   erythropoietin-mediated vasoconstriction; wound treatment.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "D-Tyr bonded to D-Trp at position 5."
FT   Misc-difference 3
FT                   /label= D-Ala.
FT   Misc-difference 5
FT                   /note= "D-Trp bonded to D-Tyr at position 1."
XX
PN   WO9325580-A.
XX
PD   23-DEC-1993.
XX
PF   17-JUN-1993;   93WO-US05788.
XX
PR   18-JUN-1992;   92US-0900620.
PR   18-JUN-1992;   92US-0900711.
XX
PA   (IMMU-) IMMUNOPHARMACEUTICS INC.
XX
PI   Balaji VN,  Chan MF;
XX
DR   WPI; 1994-007458/01.
XX
PT   New cyclic peptide(s) which modulate endothelin activity - used
PT   for treating endothelin-mediated disorders such as cardiovascular
PT   and respiratory diseases
XX
PS   Claim 2; Page 51; 58pp; English.
XX
CC   The peptide inhibits binding of endothelin-1 (ET) to ETA receptors
CC   and/or to ETB receptors.  It can be used for detecting,
CC   distinguishing and isolating ET receptor subtypes.  The peptides
CC   also act as ET antagonists and can be used to treat endothelin-
CC   mediated disorders such as hypertension, pulmonary hypertension,
CC   cardiovascular disease, bronchoconstriction, asthma, inflammatory
CC   diseases, ophthalmolgic shock, anaphylactic shock, haemorrhagic
CC   shock, gastroenteric disease, renal failure, endotoxin shock,
CC   menstrual disorders, obstretic conditions, erythropoietin-mediated
CC   vasoconstriction and wounds.
XX
SQ   Sequence   5 AA;

  Query Match             70.0%;  Score 14;  DB 15;  Length 5;
  Best Local Similarity   20.0%;  Pred. No. 7.7e+05;
  Matches    1;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           :   |
Db       1 YAAAW 5


RESULT 11
AAR69220
ID   AAR69220 standard; peptide; 5 AA.
XX
AC   AAR69220;
XX
DT   06-MAR-1995  (first entry)
XX
DE   Endothelin C-terminal peptide analog, useful as antagonist.
XX
KW   Endothelin; ET-1; receptor; antagonist.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Ac-D-Phe"
XX
PN   WO9414843-A.
XX
PD   07-JUL-1994.
XX
PF   17-DEC-1993;   93WO-US12377.
XX
PR   21-DEC-1992;   92US-0995480.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Cody WL,  Depue P,  Doherty AM,  He JX,  Taylor MD;
XX
DR   WPI; 1994-234617/28.
XX
PT   New hexa:peptide derivs. inhibiting endothelin - for treatment of
PT   e.g. renal failure, hypertension, asthma, restenosis, angina,
PT   cancer etc.
XX
PS   Claim 5; Page 119; 146pp; English.
XX
CC   Novel antagonists of endothelin are claimed which are C-terminal
CC   hexapeptides and analogs of ET-1. The first (N-terminal) amino acid
CC   of the new peptides has D-configuration. The peptides are claimed
CC   generically. The present peptide is a specifically claimed example
CC   of the generic compounds.
CC   The peptides are useful for treating hypertension, metabolic and
CC   endocrine disorders, congestive heart failure, myocardial infarction,
CC   endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute
CC   and chronic renal failure, preeclampsia, diabetes, neurological
CC   disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel
CC   disease, gastric mucosal damage, Raynaud's disease, restenosis,
CC   percutaneous transluminal coronary angioplasty, angina and cancer.
XX
SQ   Sequence   5 AA;

  Query Match             70.0%;  Score 14;  DB 15;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 7.7e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FLDIW 5


RESULT 12
AAR69260
ID   AAR69260 standard; peptide; 5 AA.
XX
AC   AAR69260;
XX
DT   07-MAR-1995  (first entry)
XX
DE   Endothelin C-terminal peptide analog, useful as antagonist.
XX
KW   Endothelin; ET-1; receptor; antagonist.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Ac-D-Phe"
XX
PN   WO9414843-A.
XX
PD   07-JUL-1994.
XX
PF   17-DEC-1993;   93WO-US12377.
XX
PR   21-DEC-1992;   92US-0995480.
XX
```

PA (WARN) WARNER LAMBERT CO.
XX
PI Cody WL, Depue P, Doherty AM, He JX, Taylor MD;
XX
DR WPI; 1994-234617/28.
XX
PT New hexa:peptide derivs. inhibiting endothelin - for treatment of
PT e.g. renal failure, hypertension, asthma, restenosis, angina,
PT cancer etc.
XX
PS Claim 5; Page 120; 146pp; English.
XX
CC Novel antagonists of endothelin are claimed which are C-terminal
CC hexapeptides and analogs of ET-1. The first (N-terminal) amino acid
CC of the new peptides has D-configuration. The peptides are claimed
CC generically. The present peptide is a specifically claimed example
CC of the generic compounds.
CC The peptides are useful for treating hypertension, metabolic and
CC endocrine disorders, congestive heart failure, myocardial infarction,
CC endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute
CC and chronic renal failure, preeclampsia, diabetes, neurological
CC disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel
CC disease, gastric mucosal damage, Raynaud's disease, restenosis,
CC percutaneous transluminal coronary angioplasty, angina and cancer.
XX
SQ Sequence 5 AA;

Query Match 70.0%; Score 14; DB 15; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 FXXXW 5
          |   |
Db      1 FDFIW 5
```

RESULT 13
AAR69210
ID AAR69210 standard; peptide; 5 AA.
XX
AC AAR69210;
XX
DT 06-MAR-1995 (first entry)
XX
DE Endothelin C-terminal peptide analog, useful as antagonist.
XX
KW Endothelin; ET-1; receptor; antagonist.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Ac-D-Phe or Ada-D-Phe, where Ada is
FT 1-adamantyl-acetyl"
XX
PN WO9414843-A.
XX
PD 07-JUL-1994.
XX
PF 17-DEC-1993; 93WO-US12377.
XX
PR 21-DEC-1992; 92US-0995480.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Cody WL, Depue P, Doherty AM, He JX, Taylor MD;
XX
DR WPI; 1994-234617/28.
XX
PT New hexa:peptide derivs. inhibiting endothelin - for treatment of
PT e.g. renal failure, hypertension, asthma, restenosis, angina,
PT cancer etc.
XX
PS Claim 5; Page 118; 146pp; English.
XX
CC Novel antagonists of endothelin are claimed which are C-terminal
CC hexapeptides and analogs of ET-1. The first (N-terminal) amino acid
CC of the new peptides has D-configuration. The peptides are claimed
CC generically. The present peptide is a specifically claimed example
CC of the generic compounds.
CC The peptides are useful for treating hypertension, metabolic and
CC endocrine disorders, congestive heart failure, myocardial infarction,
CC endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute
CC and chronic renal failure, preeclampsia, diabetes, neurological
CC disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel
CC disease, gastric mucosal damage, Raynaud's disease, restenosis,
CC percutaneous transluminal coronary angioplasty, angina and cancer.
XX
SQ Sequence 5 AA;

Query Match 70.0%; Score 14; DB 15; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.7e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 FXXXW 5
          |   |
Db      1 FDIIW 5
```

RESULT 14
AAR89837
ID AAR89837 standard; peptide; 5 AA.
XX
AC AAR89837;
XX
DT 24-JUN-1996 (first entry)
XX
DE Melanotrophic release inhibiting factor (MIF) modified peptide analogue.
XX
KW MIF; melanotrophic release inhibiting factor; modified; analogue;
KW hormone; depression; low dosage; L-propyl L-leucyl glycine;
KW melanocyte stimulating inhibitory factor.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "4-F-Phe"
FT Modified-site 2
FT /label= OTHER
FT /note= "Homo-Pro"
FT Modified-site 5
FT /label= OTHER
FT /note= "amidated"
XX
PN WO9530430-A1.
XX
PD 16-NOV-1995.
XX
PF 02-MAY-1995; 95WO-US05560.
XX
PR 04-MAY-1994; 94US-0238089.
XX
PA (INNA-) INNAPHARMA INC.
XX
PI Abajian HB, Hlavka JJ, Noble JF;
XX
DR WPI; 1995-403936/51.
XX
PT New tri-, tetra-, penta- and poly-peptide cpds. - based on the
PT tri:peptide hormone melanocyte stimulating inhibitory factor, used
PT for treating depression
XX
PS Claim 67; Page 32; 138pp; English.
XX

```
CC   AAR89786-R89858 are small peptide compounds based on the tripeptide
CC   hormone melanotrophic release inhibiting factor (MIF), also known as
CC   L-propyl L-leucyl glycine and melanocyte stimulating inhibitory
CC   factor. The peptides are used for treating depression and can be
CC   administered so as to achieve a circulating plasma level of 30-90 mg
CC   per average human adult. The peptides show greater anti-depressant
CC   activity than MIF. They can be administered at lower dosage than
CC   known anti-depressants which reduces potential deleterious side
CC   effects.
XX
SQ   Sequence   5 AA;

  Query Match             70.0%;  Score 14;  DB 16;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 7.7e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           ||  |
Db       1 FXIGW 5


RESULT 15
AAR89842
ID   AAR89842 standard; peptide; 5 AA.
XX
AC   AAR89842;
XX
DT   24-JUN-1996  (first entry)
XX
DE   Melanotrophic release inhibiting factor (MIF) modified peptide analogue.
XX
KW   MIF; melanotrophic release inhibiting factor; modified; analogue;
KW   hormone; depression; low dosage; L-propyl L-leucyl glycine;
KW   melanocyte stimulating inhibitory factor.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /label= OTHER
FT                   /note= "4-F-Phe"
FT   Modified-site   2
FT                   /label= OTHER
FT                   /note= "Homo-Pro"
FT   Modified-site   5
FT                   /label= OTHER
FT                   /note= "amidated"
XX
PN   WO9530430-A1.
XX
PD   16-NOV-1995.
XX
PF   02-MAY-1995;   95WO-US05560.
XX
PR   04-MAY-1994;   94US-0238089.
XX
PA   (INNA-) INNAPHARMA INC.
XX
PI   Abajian HB,  Hlavka JJ,  Noble JF;
XX
DR   WPI; 1995-403936/51.
XX
PT   New tri-, tetra-, penta- and poly-peptide cpds. - based on the
PT   tri:peptide hormone melanocyte stimulating inhibitory factor, used
PT   for treating depression
XX
PS   Claim 68; Page 32; 138pp; English.
XX
CC   AAR89786-R89858 are small peptide compounds based on the tripeptide
CC   horhone melanotrophic release inhibiting factor (MIF), also known as
CC   L-propyl L-leucyl glycine and melanocyte stimulating inhibitory
CC   factor. The peptides are used for treating depression and can be
CC   administered so as to achieve a circulating plasma level of 30-90 mg
CC   per average human adult. The peptides show greater anti-depressant
CC   activity than MIF. They can be administered at lower dosage than
CC   known anti-depressants which reduces potential deleterious side
CC   effects.
XX
SQ   Sequence   5 AA;

  Query Match             70.0%;  Score 14;  DB 16;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 7.7e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           ||  |
Db       1 FXRGW 5


Search completed: January 29, 2003, 14:22:04
Job time : 35 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:22:59 ; Search time 10 Seconds
(without alignments)
10.089 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 2031

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14	70.0	5	10	US-09-214-371-2	Sequence 2, Appli
2	14	70.0	5	10	US-09-281-717-3	Sequence 3, Appli
3	11	55.0	5	8	US-08-239-765B-4	Sequence 4, Appli
4	11	55.0	5	8	US-08-484-409-35	Sequence 35, Appl
5	11	55.0	5	8	US-08-424-550B-228	Sequence 228, App
6	11	55.0	5	8	US-08-424-550B-469	Sequence 469, App
7	11	55.0	5	9	US-09-995-749A-14	Sequence 14, Appl
8	11	55.0	5	9	US-09-764-884-2	Sequence 2, Appli
9	11	55.0	5	9	US-09-895-593-15	Sequence 15, Appl
10	11	55.0	5	9	US-09-895-593-16	Sequence 16, Appl
11	11	55.0	5	9	US-09-423-800-62	Sequence 62, Appl
12	11	55.0	5	9	US-09-764-857-2	Sequence 2, Appli
13	11	55.0	5	9	US-09-860-670-2	Sequence 2, Appli
14	11	55.0	5	9	US-09-968-561A-211	Sequence 211, App
15	11	55.0	5	9	US-09-968-561A-217	Sequence 217, App
16	11	55.0	5	9	US-09-981-876-2	Sequence 2, Appli
17	11	55.0	5	9	US-09-984-245-2	Sequence 2, Appli
18	11	55.0	5	9	US-09-764-868-2	Sequence 2, Appli
19	11	55.0	5	9	US-10-014-485A-79	Sequence 79, Appl
20	11	55.0	5	9	US-10-104-019-42	Sequence 42, Appl
21	11	55.0	5	9	US-09-764-904-2	Sequence 2, Appli
22	11	55.0	5	9	US-09-852-797-2	Sequence 2, Appli
23	11	55.0	5	9	US-09-964-992A-11	Sequence 11, Appl
24	11	55.0	5	9	US-10-035-349-2	Sequence 2, Appli
25	11	55.0	5	9	US-10-035-349-8	Sequence 8, Appli
26	11	55.0	5	9	US-09-828-272A-6	Sequence 6, Appli
27	11	55.0	5	9	US-10-042-141-2	Sequence 2, Appli
28	11	55.0	5	9	US-10-059-749-57	Sequence 57, Appl
29	11	55.0	5	9	US-10-059-749-63	Sequence 63, Appl
30	11	55.0	5	9	US-10-059-749-69	Sequence 69, Appl
31	11	55.0	5	9	US-10-079-625-6	Sequence 6, Appli
32	11	55.0	5	9	US-10-029-301-4	Sequence 4, Appli
33	11	55.0	5	9	US-10-074-956-6	Sequence 6, Appli
34	11	55.0	5	9	US-10-078-059-5	Sequence 5, Appli
35	11	55.0	5	9	US-10-087-195-3	Sequence 3, Appli
36	11	55.0	5	9	US-09-320-713-14	Sequence 14, Appl
37	11	55.0	5	9	US-09-774-639-2	Sequence 2, Appli
38	11	55.0	5	9	US-09-798-889-2	Sequence 2, Appli
39	11	55.0	5	9	US-09-201-396-7	Sequence 7, Appli
40	11	55.0	5	9	US-10-105-930-21	Sequence 21, Appl
41	11	55.0	5	9	US-10-105-930-57	Sequence 57, Appl
42	11	55.0	5	9	US-10-105-930-58	Sequence 58, Appl
43	11	55.0	5	9	US-10-105-930-59	Sequence 59, Appl
44	11	55.0	5	9	US-10-105-930-60	Sequence 60, Appl
45	11	55.0	5	9	US-10-105-930-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-09-214-371-2
; Sequence 2, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: Where Xaa may be any amino acid
US-09-214-371-2

Query Match 70.0%; Score 14; DB 10; Length 5;
Best Local Similarity 80.0%; Pred. No. 9.9e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXXXW 5
||| |
Db 1 FXXLW 5

RESULT 2
US-09-281-717-3
; Sequence 3, Application US/09281717

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; Patent No. US20020061539A1
; GENERAL INFORMATION:
;  APPLICANT: Baxter, John D.
;  APPLICANT: Darimont, Beatrice
;  APPLICANT: Feng, Weijun
;  APPLICANT: Fletterick, Robert J.
;  APPLICANT: Kushner, Peter J.
;  APPLICANT: Wagner, Richard L.
;  APPLICANT: West, Brian
;  APPLICANT: Yamamoto, Keith R.
;  TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
;  TITLE OF INVENTION: COACTIVATOR BINDING
;  FILE REFERENCE: UCAL-253/02US
;  CURRENT APPLICATION NUMBER: US/09/281,717
;  CURRENT FILING DATE: 1999-03-30
;  EARLIER APPLICATION NUMBER: US 60/079,956
;  EARLIER FILING DATE: 1998-03-30
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (2)..(3)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-281-717-3

  Query Match             70.0%;  Score 14;  DB 10;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 9.9e+04;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
            ||| |
Db       1 FXXLW 5


RESULT 3
US-08-239-765B-4
; Sequence 4, Application US/08239765B
; Patent No. US20020026650A1
;  GENERAL INFORMATION:
;    APPLICANT:  Savakis, Charalambos
;    APPLICANT:  Franz, Gerald H.
;    APPLICANT:  Loukeris, Athanasios
;    TITLE OF INVENTION:  Eukaryotic Transposable Element
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/239,765B
;      FILING DATE:  09-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/946,237
;      FILING DATE:  14-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  BTT92-01Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-239-765B-4

  Query Match             55.0%;  Score 11;  DB 8;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
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Db       3 W 3


RESULT 4
US-08-484-409-35
; Sequence 35, Application US/08484409
; Patent No. US20020076412A1
;  GENERAL INFORMATION:
;    APPLICANT:  Steinman, Lawrence
;    APPLICANT:  Zamvil, Scott
;    TITLE OF INVENTION:  METHODS FOR MODULATING THE IMMUNE SYSTEM
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,409
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  690068.409C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-484-409-35

  Query Match             55.0%;  Score 11;  DB 8;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
            |
Db       2 W 2


RESULT 5
US-08-424-550B-228
; Sequence 228, Application US/08424550B
; Patent No. US20020119447A1
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  JOHN N. SIMONS
;    APPLICANT:  TAMI J. PILOT-MATIAS
;    APPLICANT:  GEORGE J. DAWSON
;    APPLICANT:  GEORGE G. SCHLAUDER
;    APPLICANT:  SURESH M. DESAI
;    APPLICANT:  THOMAS P. LEARY
;    APPLICANT:  ANTHONY SCOTT MUERHOFF
;    APPLICANT:  JAMES C. ERKER
;    APPLICANT:  SHERI L. BUIJK
;    APPLICANT:  ISA K. MUSHAHWAR
;    TITLE OF INVENTION:  NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
;    TITLE OF INVENTION:  REAGENTS AND METHODS FOR THEIR USE
;    NUMBER OF SEQUENCES:  716
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ABBOTT LABORATORIES  D377/AP6D
;      STREET:  100 ABBOTT PARK ROAD
;      CITY:  ABBOTT PARK
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/424,550B
;      FILING DATE:
;      CLASSIFICATION:  435435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  POREMBSKI, PRISCILLA E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5527.PC.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-6365
;      TELEFAX:  708-938-2623
;  INFORMATION FOR SEQ ID NO:  228:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-424-550B-228

  Query Match             55.0%;  Score 11;  DB 8;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
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Db       4 W 4


RESULT 6
US-08-424-550B-469
; Sequence 469, Application US/08424550B
; Patent No. US20020119447A1
;  GENERAL INFORMATION:
;    APPLICANT:  JOHN N. SIMONS
;    APPLICANT:  TAMI J. PILOT-MATIAS
;    APPLICANT:  GEORGE J. DAWSON
;    APPLICANT:  GEORGE G. SCHLAUDER
;    APPLICANT:  SURESH M. DESAI
;    APPLICANT:  THOMAS P. LEARY
;    APPLICANT:  ANTHONY SCOTT MUERHOFF
;    APPLICANT:  JAMES C. ERKER
;    APPLICANT:  SHERI L. BUIJK
;    APPLICANT:  ISA K. MUSHAHWAR
;    TITLE OF INVENTION:  NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
;    TITLE OF INVENTION:  REAGENTS AND METHODS FOR THEIR USE
;    NUMBER OF SEQUENCES:  716
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ABBOTT LABORATORIES  D377/AP6D
;      STREET:  100 ABBOTT PARK ROAD
;      CITY:  ABBOTT PARK
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/424,550B
;      FILING DATE:
;      CLASSIFICATION:  435435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  POREMBSKI, PRISCILLA E.
;      REGISTRATION NUMBER:  33,207
;      REFERENCE/DOCKET NUMBER:  5527.PC.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  708-937-6365
;      TELEFAX:  708-938-2623
;  INFORMATION FOR SEQ ID NO:  469:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-424-550B-469

  Query Match             55.0%;  Score 11;  DB 8;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
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Db       5 W 5


RESULT 7
US-09-995-749A-14
; Sequence 14, Application US/09995749A
; Patent No. US20020155568A1
; GENERAL INFORMATION:
;  APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
;  APPLICANT:  DIJKHUIZEN, LUBBERT
;  APPLICANT:  RAHAOUI, HAKIM
;  APPLICANT:  LEER, ROBERT-JAN
;  TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
;  FILE REFERENCE: BO43388-CIP
;  CURRENT APPLICATION NUMBER: US/09/995,749A
;  CURRENT FILING DATE:  2001-11-29
;  PRIOR APPLICATION NUMBER: 09/604,957
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: EPO 00201871.1
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Neisseria polysaccharea
US-09-995-749A-14

  Query Match             55.0%;  Score 11;  DB 9;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
           |
Db       2 W 2


RESULT 8
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US-09-764-884-2
; Sequence 2, Application US/09764884
; Patent No. US20020161208A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ03
;  CURRENT APPLICATION NUMBER: US/09/764,884
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Site
;   LOCATION: (3)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-09-764-884-2

  Query Match            55.0%;  Score 11;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
          |
Db      1 W 1


RESULT 9
US-09-895-593-15
; Sequence 15, Application US/09895593
; Patent No. US20020160949A1
; GENERAL INFORMATION:
;  APPLICANT: Pandey, Akhilesh
;  APPLICANT:  Ozaki, Katsutoshi
;  APPLICANT:  Baumann, Heinz
;  APPLICANT:  Levin, Steven D.
;  APPLICANT:  Farr, Andrew G.
;  APPLICANT:  Ziegler, Steven F.
;  APPLICANT:  Leonard, Warren J.
;  APPLICANT:  Lodish, Harvey F.
;  TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
;  TITLE OF INVENTION:  Uses Thereof
;  FILE REFERENCE: 00-514-E
;  CURRENT APPLICATION NUMBER: US/09/895,593
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: 60/215,658
;  PRIOR FILING DATE: 2000-06-28
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Type I
;   OTHER INFORMATION: cytokine receptor conserved motif
;   NAME/KEY: UNSURE
;   LOCATION: (3)
;   OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid
US-09-895-593-15

  Query Match            55.0%;  Score 11;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
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Db      1 W 1


RESULT 10
US-09-895-593-16
; Sequence 16, Application US/09895593
; Patent No. US20020160949A1
; GENERAL INFORMATION:
;  APPLICANT: Pandey, Akhilesh
;  APPLICANT:  Ozaki, Katsutoshi
;  APPLICANT:  Baumann, Heinz
;  APPLICANT:  Levin, Steven D.
;  APPLICANT:  Farr, Andrew G.
;  APPLICANT:  Ziegler, Steven F.
;  APPLICANT:  Leonard, Warren J.
;  APPLICANT:  Lodish, Harvey F.
;  TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
;  TITLE OF INVENTION:  Uses Thereof
;  FILE REFERENCE: 00-514-E
;  CURRENT APPLICATION NUMBER: US/09/895,593
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: 60/215,658
;  PRIOR FILING DATE: 2000-06-28
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Motif
;   OTHER INFORMATION: replacing type I cytokine receptor conserved motif
;   OTHER INFORMATION: in murine TSLPR polypeptide
US-09-895-593-16

  Query Match            55.0%;  Score 11;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
          |
Db      1 W 1


RESULT 11
US-09-423-800-62
; Sequence 62, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
;  APPLICANT:  SATO, KOH
;  APPLICANT:  TSUNENARI, TOSHIAKI
;  APPLICANT:  ISHII, KIMIE
;  TITLE OF INVENTION:  CACHEXIA REMEDY
;  FILE REFERENCE:  04853-0036
;  CURRENT APPLICATION NUMBER: US/09/423,800
;  CURRENT FILING DATE:  1999-11-12
;  PRIOR APPLICATION NUMBER:  PCT/JP98/02116
;  PRIOR FILING DATE:  1998-05-13
;  PRIOR APPLICATION NUMBER:  JP 125505/1997
;  PRIOR FILING DATE:  1997-05-15
;  PRIOR APPLICATION NUMBER:  JP 194445/1997
;  PRIOR FILING DATE:  1997-07-18
;  NUMBER OF SEQ ID NOS:  87
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 62
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-423-800-62

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  Best Local Similarity  100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
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Db      3 W 3


RESULT 12
US-09-764-857-2
; Sequence 2, Application US/09764857
; Patent No. US20020164685A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ11
;  CURRENT APPLICATION NUMBER: US/09/764,857
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Site
;   LOCATION: (3)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-09-764-857-2

  Query Match            55.0%;  Score 11;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
          |
Db      1 W 1


RESULT 13
US-09-860-670-2
; Sequence 2, Application US/09860670
; Patent No. US20020165137A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PA127P1
;  CURRENT APPLICATION NUMBER: US/09/860,670
;  CURRENT FILING DATE:  2001-05-21
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 289
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Site
;   LOCATION: (3)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
US-09-860-670-2

  Query Match            55.0%;  Score 11;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
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Db      1 W 1


RESULT 14
US-09-968-561A-211
; Sequence 211, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
;  APPLICANT: Tomlinson, Ian M
;  APPLICANT:  Winter, Gregory
;  TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
;  FILE REFERENCE: 8039/1073B
;  CURRENT APPLICATION NUMBER: US/09/968,561A
;  CURRENT FILING DATE:  2001-10-01
;  PRIOR APPLICATION NUMBER: GB 9722131.1
;  PRIOR FILING DATE: 1997-10-20
;  PRIOR APPLICATION NUMBER: US 60/065,248
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: US 60/066,729
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: PCT/GB98/03135
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: US 09/511,939
;  PRIOR FILING DATE: 2000-02-24
;  NUMBER OF SEQ ID NOS: 350
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-968-561A-211

  Query Match            55.0%;  Score 11;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
          |
Db      5 W 5


RESULT 15
US-09-968-561A-217
; Sequence 217, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
;  APPLICANT: Tomlinson, Ian M
;  APPLICANT:  Winter, Gregory
;  TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
;  FILE REFERENCE: 8039/1073B
;  CURRENT APPLICATION NUMBER: US/09/968,561A
;  CURRENT FILING DATE:  2001-10-01
;  PRIOR APPLICATION NUMBER: GB 9722131.1
;  PRIOR FILING DATE: 1997-10-20
;  PRIOR APPLICATION NUMBER: US 60/065,248
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: US 60/066,729
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: PCT/GB98/03135
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: US 09/511,939
;  PRIOR FILING DATE: 2000-02-24
;  NUMBER OF SEQ ID NOS: 350
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-968-561A-217

  Query Match            55.0%;  Score 11;  DB 9;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 9.9e+04;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
          |
Db      5 W 5


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Job time : 10 secs
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:22:09 ; Search time 131 Seconds
(without alignments)
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Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

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Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 42829

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15	75.0	5	1	PCT-US99-02405-11	Sequence 11, Appl
2	15	75.0	5	1	PCT-US99-26277-114	Sequence 114, App
3	15	75.0	5	20	US-09-601-558-11	Sequence 11, Appl
4	15	75.0	5	22	US-09-831-047B-114	Sequence 114, App
5	15	75.0	5	22	US-09-831-047C-114	Sequence 114, App
6	15	75.0	5	22	US-09-894-594-11	Sequence 11, Appl
7	14	70.0	5	1	PCT-US01-20969-3	Sequence 3, Appli
8	14	70.0	5	13	US-08-981-122-37	Sequence 37, Appl
9	14	70.0	5	16	US-09-214-371-2	Sequence 2, Appli
10	14	70.0	5	16	US-09-281-717-3	Sequence 3, Appli
11	14	70.0	5	18	US-09-403-440A-1	Sequence 1, Appli
12	14	70.0	5	18	US-09-403-440A-4	Sequence 4, Appli
13	14	70.0	5	20	US-09-609-361-3	Sequence 3, Appli
14	14	70.0	5	23	US-09-957-806A-226	Sequence 226, App
15	13	65.0	5	4	US-08-064-111B-22	Sequence 22, Appl
16	13	65.0	5	8	US-08-481-896-99	Sequence 99, Appl
17	13	65.0	5	13	US-08-981-122-2	Sequence 2, Appli
18	13	65.0	5	17	US-09-392-941-83	Sequence 83, Appl
19	13	65.0	5	17	US-09-392-941A-169	Sequence 169, App
20	12	60.0	5	1	PCT-US02-04431-4	Sequence 4, Appli
21	12	60.0	5	1	PCT-US02-29060-84	Sequence 84, Appl
22	12	60.0	5	1	PCT-US98-22335-320	Sequence 320, App
23	12	60.0	5	9	US-08-591-447-32	Sequence 32, Appl
24	12	60.0	5	9	US-08-591-447A-32	Sequence 32, Appl
25	12	60.0	5	11	US-08-753-750-39	Sequence 39, Appl
26	12	60.0	5	11	US-08-753-750A-39	Sequence 39, Appl
27	12	60.0	5	11	US-08-753-750B-39	Sequence 39, Appl
28	12	60.0	5	13	US-08-961-707-320	Sequence 320, App
29	12	60.0	5	19	US-09-584-501A-39	Sequence 39, Appl
30	12	60.0	5	23	US-09-953-592-84	Sequence 84, Appl
31	12	60.0	5	24	US-10-052-578-320	Sequence 320, App
32	12	60.0	5	24	US-10-053-520-320	Sequence 320, App
33	12	60.0	5	26	US-10-243-613-84	Sequence 84, Appl
34	11	55.0	5	1	PCT-US00-00807-17	Sequence 17, Appl
35	11	55.0	5	1	PCT-US00-00903-2	Sequence 2, Appli
36	11	55.0	5	1	PCT-US00-01602-223	Sequence 223, App
37	11	55.0	5	1	PCT-US00-02041-14	Sequence 14, Appl
38	11	55.0	5	1	PCT-US00-03062-2	Sequence 2, Appli
39	11	55.0	5	1	PCT-US00-03062-2	Sequence 2, Appli
40	11	55.0	5	1	PCT-US00-05881-838	Sequence 838, App
41	11	55.0	5	1	PCT-US00-05882-1686	Sequence 1686, Ap
42	11	55.0	5	1	PCT-US00-05883-1548	Sequence 1548, Ap
43	11	55.0	5	1	PCT-US00-05918-888	Sequence 888, App
44	11	55.0	5	1	PCT-US00-05988-1882	Sequence 1882, Ap
45	11	55.0	5	1	PCT-US00-05989-920	Sequence 920, App

ALIGNMENTS

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RESULT 1
PCT-US99-02405-11
; Sequence 11, Application PC/TUS9902405
; GENERAL INFORMATION:
;  APPLICANT: Trustees of the University of Pennsylvania
;  TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens
;  FILE REFERENCE: upn3544
;  CURRENT APPLICATION NUMBER: PCT/US99/02405
;  CURRENT FILING DATE: 1999-02-04
;  EARLIER APPLICATION NUMBER: 60/073,690
;  EARLIER FILING DATE: 1998-02-04
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US99-02405-11

  Query Match             75.0%;  Score 15;  DB 1;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 4.2e+06;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FSLLW 5
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RESULT 2
PCT-US99-26277-114
; Sequence 114, Application PC/TUS9926277
; GENERAL INFORMATION:
;  APPLICANT: The Wistar Institute of Anatomy and Biology
;  APPLICANT: The Trustees of the University of Pennsylvania
;  APPLICANT: Blaszczyk-Thurin, Magdalena
;  APPLICANT: Keiber-Emmons, Thomas
;  TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
;  FILE REFERENCE: WST93PCT
;  CURRENT APPLICATION NUMBER: PCT/US99/26277
;  CURRENT FILING DATE: 1999-11-05
;  EARLIER APPLICATION NUMBER: 60/107,478
;  EARLIER FILING DATE: 1998-11-06
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: peptido-mimetic of a Lewis antigen
PCT-US99-26277-114

  Query Match             75.0%;  Score 15;  DB 1;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 4.2e+06;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FSLLW 5


RESULT 3
US-09-601-558-11
; Sequence 11, Application US/09601558
; GENERAL INFORMATION:
;  APPLICANT:  Kieber-Emmons, Thomas
;  APPLICANT:  The Trustees of the University of Pennsylvania
;  TITLE OF INVENTION:  Peptide Mimotopes Of Carbohydrate Antigens
;  FILE REFERENCE:  UPN3567
;  CURRENT APPLICATION NUMBER: US/09/601,558
;  CURRENT FILING DATE:  2000-08-03
;  PRIOR APPLICATION NUMBER:  PCT/US99/02405
;  PRIOR FILING DATE:  1999-02-04
;  PRIOR APPLICATION NUMBER:  60/073,690
;  PRIOR FILING DATE:  1998-02-04
;  NUMBER OF SEQ ID NOS:  60
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-601-558-11

  Query Match             75.0%;  Score 15;  DB 20;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 4.2e+06;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FSLLW 5


RESULT 4
US-09-831-047B-114
; Sequence 114, Application US/09831047B
; GENERAL INFORMATION:
;  APPLICANT:  The Wistar Institute of Anatomy and Biology
;  APPLICANT:  The Trustees of the University of Pennsylvania
;  APPLICANT:  Blaszczyk-Thurin, Magdalena
;  APPLICANT:  Kieber-Emmons, Thomas
;  TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
;  FILE REFERENCE: WST93AUSA
;  CURRENT APPLICATION NUMBER: US/09/831,047B
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: 60/107,478
;  PRIOR FILING DATE: 1998-11-06
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: peptido-mimetic of a Lewis antigen
US-09-831-047B-114

  Query Match             75.0%;  Score 15;  DB 22;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 4.2e+06;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
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Db       1 FSLLW 5


RESULT 5
US-09-831-047C-114
; Sequence 114, Application US/09831047C
; GENERAL INFORMATION:
;  APPLICANT: The Wistar Institute of Anatomy and Biology
;  APPLICANT:  The Trustees of the University of Pennsylvania
;  APPLICANT:  Blaszczyk-Thurin, Magdalena
;  APPLICANT:  Kieber-Emmons, Thomas
;  TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
;  FILE REFERENCE: WST93AUSA
;  CURRENT APPLICATION NUMBER: US/09/831,047C
;  CURRENT FILING DATE:  2001-05-03
;  PRIOR APPLICATION NUMBER: 60/107,478
;  PRIOR FILING DATE: 1998-11-06
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 114
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: peptido-mimetic of a Lewis antigen
US-09-831-047C-114

  Query Match             75.0%;  Score 15;  DB 22;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 4.2e+06;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FSLLW 5


RESULT 6
US-09-894-594-11
; Sequence 11, Application US/09894594
; GENERAL INFORMATION:
;  APPLICANT: Kieber-Emmons, Thomas
;  APPLICANT:  Weiner, David B.
;  APPLICANT:  Monzavi-Karbassi, Behjatolah
;  TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules E
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: UPN-3984
;  CURRENT APPLICATION NUMBER: US/09/894,594
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: 09/601,558
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;  PRIOR FILING DATE: 2000-11-07
;  PRIOR APPLICATION NUMBER: PCT/US99/02405
;  PRIOR FILING DATE: 1999-02-04
;  PRIOR APPLICATION NUMBER: 60/073,690
;  PRIOR FILING DATE: 1998-02-04
;  PRIOR APPLICATION NUMBER: 60/214,517
;  PRIOR FILING DATE: 2000-06-28
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Novel Sequence
US-09-894-594-11

  Query Match           75.0%;  Score 15;  DB 22;  Length 5;
  Best Local Similarity  40.0%;  Pred. No. 4.2e+06;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      1 FSLLW 5


RESULT 7
PCT-US01-20969-3
; Sequence 3, Application PC/TUS0120969
; GENERAL INFORMATION:
;  APPLICANT: GUY, RODNEY
;  APPLICANT:  BAXTER, JOHN
;  APPLICANT:  DARIMONT, BEATRICE
;  APPLICANT:  FENG, WEIJUN
;  APPLICANT:  ROBERT, FLETTERICK
;  APPLICANT:  PETER, KUSHNER
;  APPLICANT:  RICHARD, WAGNER
;  APPLICANT:  BRIAN, WEST
;  APPLICANT:  YAMAMOTO, KEITH
;  APPLICANT:  GEISTLINGER, TIMOTHY
;  APPLICANT:  ARNOLD, JAMES
;  APPLICANT:  KUNTZ, IRWIN
;  TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
;  TITLE OF INVENTION:  ACTIVITY
;  FILE REFERENCE: 9811-016-228
;  CURRENT APPLICATION NUMBER: PCT/US01/20969
;  CURRENT FILING DATE:  2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/609,361
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 60/079,965
;  PRIOR FILING DATE: 1998-03-30
;  PRIOR APPLICATION NUMBER: US 60/113,146
;  PRIOR FILING DATE: 1998-12-16
;  PRIOR APPLICATION NUMBER: US09/281,717
;  PRIOR FILING DATE: 1999-03-30
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2)..(3)
;   OTHER INFORMATION: Xaa is any amino acid
PCT-US01-20969-3

  Query Match           70.0%;  Score 14;  DB 1;  Length 5;
  Best Local Similarity  80.0%;  Pred. No. 4.2e+06;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          ||| |
Db      1 FXXLW 5


RESULT 8
US-08-981-122-37
; Sequence 37, Application US/08981122A
; GENERAL INFORMATION:
;  APPLICANT: Hatanaka, Yoshihiro
;  APPLICANT: Aritomi, Masaharu
;  TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/08/981,122A
;  CURRENT FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: JP 7-176904
;  EARLIER FILING DATE: 1995-06-21
;  EARLIER APPLICATION NUMBER: PCT/JP96/01734
;  EARLIER FILING DATE: 1996-06-21
;  NUMBER OF SEQ ID NOS: 90
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: 5
;   FEATURE:
;   OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-
;   OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic pep
;   OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
US-08-981-122-37

  Query Match           70.0%;  Score 14;  DB 13;  Length 5;
  Best Local Similarity  40.0%;  Pred. No. 4.2e+06;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      1 FFFRW 5


RESULT 9
US-09-214-371-2
; Sequence 2, Application US/09214371B
; GENERAL INFORMATION:
;  APPLICANT:  Lane, David
;  APPLICANT:  Bottger, Volker
;  APPLICANT:  Bottger, Angelica
;  APPLICANT:  Picksley, Stephen
;  APPLICANT:  Chene, Patrick
;  APPLICANT:  Hochkeppel, Heinz-Kurt
;  APPLICANT:  Garcia-Echeverria, Carlos
;  APPLICANT:  Furet, Pascal
;  TITLE OF INVENTION:  Inhibitors of the Interaction of P53 and MDM2
;  FILE REFERENCE:  4-20937/A/PCT
;  CURRENT APPLICATION NUMBER: US/09/214,371B
;  CURRENT FILING DATE:  1999-03-26
;  PRIOR APPLICATION NUMBER:  PCT/EP97/03549
;  PRIOR FILING DATE:  1997-07-04
;  NUMBER OF SEQ ID NOS:  83
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:peptide
;   OTHER INFORMATION: Where Xaa may be any amino acid
US-09-214-371-2

  Query Match           70.0%;  Score 14;  DB 16;  Length 5;
  Best Local Similarity  80.0%;  Pred. No. 4.2e+06;
```

```
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           ||| |
Db       1 FXXLW 5


RESULT 10
US-09-281-717-3
; Sequence 3, Application US/09281717
; GENERAL INFORMATION:
;  APPLICANT: Baxter, John D.
;  APPLICANT: Darimont, Beatrice
;  APPLICANT: Feng, Weijun
;  APPLICANT: Fletterick, Robert J.
;  APPLICANT: Kushner, Peter J.
;  APPLICANT: Wagner, Richard L.
;  APPLICANT: West, Brian
;  APPLICANT: Yamamoto, Keith R.
;  TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
;  TITLE OF INVENTION: COACTIVATOR BINDING
;  FILE REFERENCE: UCAL-253/02US
;  CURRENT APPLICATION NUMBER: US/09/281,717
;  CURRENT FILING DATE: 1999-03-30
;  EARLIER APPLICATION NUMBER: US 60/079,956
;  EARLIER FILING DATE: 1998-03-30
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (2)..(3)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-281-717-3

  Query Match             70.0%;  Score 14;  DB 16;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 4.2e+06;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           ||| |
Db       1 FXXLW 5


RESULT 11
US-09-403-440A-1
; Sequence 1, Application US/09403440A
; GENERAL INFORMATION:
;  APPLICANT: Lane, David Philip
;  TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO
;  TITLE OF INVENTION:  INHIBITING THE INTERACTION OF p53 AND MDM2
;  FILE REFERENCE: MEWB25.001APC
;  CURRENT APPLICATION NUMBER: US/09/403,440A
;  CURRENT FILING DATE:  2000-01-19
;  PRIOR APPLICATION NUMBER: PCT/GB98/01144
;  PRIOR FILING DATE: 1998-04-20
;  PRIOR APPLICATION NUMBER: GB 9708092.3
;  PRIOR FILING DATE: 1997-04-22
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: This represents a consensus sequence representing
;   OTHER INFORMATION: humans and mice.
;   NAME/KEY: UNSURE
;   LOCATION: 2, 3
;   OTHER INFORMATION: Xaa = any amino acid
US-09-403-440A-1

  Query Match             70.0%;  Score 14;  DB 18;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 4.2e+06;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           ||| |
Db       1 FXXLW 5


RESULT 12
US-09-403-440A-4
; Sequence 4, Application US/09403440A
; GENERAL INFORMATION:
;  APPLICANT: Lane, David Philip
;  TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO
;  TITLE OF INVENTION:  INHIBITING THE INTERACTION OF p53 AND MDM2
;  FILE REFERENCE: MEWB25.001APC
;  CURRENT APPLICATION NUMBER: US/09/403,440A
;  CURRENT FILING DATE:  2000-01-19
;  PRIOR APPLICATION NUMBER: PCT/GB98/01144
;  PRIOR FILING DATE: 1998-04-20
;  PRIOR APPLICATION NUMBER: GB 9708092.3
;  PRIOR FILING DATE: 1997-04-22
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: This represents a consensus sequence representing
;   OTHER INFORMATION: humans and mice.
;   NAME/KEY: UNSURE
;   LOCATION: 2, 3, 4
;   OTHER INFORMATION: Xaa = any amino acid
US-09-403-440A-4

  Query Match             70.0%;  Score 14;  DB 18;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |||||
Db       1 FXXXW 5


RESULT 13
US-09-609-361-3
; Sequence 3, Application US/09609361
; GENERAL INFORMATION:
;  APPLICANT: GUY, RODNEY
;  APPLICANT:  BAXTER, JOHN
;  APPLICANT:  DARIMONT, BEATRICE
;  APPLICANT:  FENG, WEIJUN
;  APPLICANT:  ROBERT, FLETTERICK
;  APPLICANT:  PETER, KUSHNER
;  APPLICANT:  RICHARD, WAGNER
;  APPLICANT:  BRIAN, WEST
;  APPLICANT:  YAMAMOTO, KEITH
;  APPLICANT:  GEISTLINGER, TIMOTHY
;  APPLICANT:  ARNOLD, JAMES
;  APPLICANT:  KUNTZ, IRWIN
;  TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR ACTIVITY
;  FILE REFERENCE: 9811-016-999
;  CURRENT APPLICATION NUMBER: US/09/609,361
;  CURRENT FILING DATE:  2000-06-30
;  PRIOR APPLICATION NUMBER: US 60/079,965
;  PRIOR FILING DATE: 1998-03-30
;  PRIOR APPLICATION NUMBER: US 60/113,146
;  PRIOR FILING DATE: 1998-12-16
;  PRIOR APPLICATION NUMBER: US09/281,717
```

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;  PRIOR FILING DATE: 1999-03-30
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2)..(3)
;   OTHER INFORMATION: Xaa is any amino acid
US-09-609-361-3

  Query Match             70.0%;  Score 14;  DB 20;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 4.2e+06;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           ||| |
Db       1 FXXLW 5


RESULT 14
US-09-957-806A-226
; Sequence 226, Application US/09957806A
; GENERAL INFORMATION:
;  APPLICANT: Roggen, Erwin
;  APPLICANT:  Ernst, Steffen
;  APPLICANT:  Svendsen, Allan
;  APPLICANT:  Friis, Esben
;  APPLICANT:  Osten, Claus
;  TITLE OF INVENTION: PROTEIN VARIANTS HAVING MODIFIED IMMUNOGENICITY
;  FILE REFERENCE: 10021.204-US
;  CURRENT APPLICATION NUMBER: US/09/957,806A
;  CURRENT FILING DATE:  2001-09-21
;  NUMBER OF SEQ ID NOS: 248
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 226
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Betula
US-09-957-806A-226

  Query Match             70.0%;  Score 14;  DB 23;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 4.2e+06;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |  |
Db       1 FIKLW 5


RESULT 15
US-08-064-111B-22
; Sequence 22, Application US/08064111B
;  GENERAL INFORMATION:
;     APPLICANT:  Kemp, Bruce E.
;     APPLICANT:  Nicholson, Geoffrey C.
;     APPLICANT:  Martin, Thomas J.
;     APPLICANT:  Fenton, Anna J.
;     APPLICANT:  Hammonds, R. Glenn
;     TITLE OF INVENTION:  COMPOUNDS AND COMPOSITIONS WHICH INHIBIT
;     TITLE OF INVENTION:  BONE RESORPTION
;     NUMBER OF SEQUENCES:  26
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert,
;       ADDRESSEE:  Attn: W.H. Dreger
;       STREET:  4 Embarcadero Center, Suite 3400
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  United States
;       ZIP:  94111-4187
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/064,111B
;       FILING DATE:  12-AUG-1993
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/AU91/00580
;       FILING DATE:  13-DEC-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  AU PK9567
;       FILING DATE:  19-NOV-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  AU PK3879
;       FILING DATE:  13-DEC-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Dreger, Walter H.
;       REGISTRATION NUMBER:  24,190
;       REFERENCE/DOCKET NUMBER:  A-58456/WHD
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 781-1989
;       TELEFAX:  (415) 398-3249
;       TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  5 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-064-111B-22

  Query Match             65.0%;  Score 13;  DB 4;  Length 5;
  Best Local Similarity   20.0%;  Pred. No. 4.2e+06;
  Matches    1;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           :   |
Db       1 YRSAW 5


Search completed: January 29, 2003, 14:25:57
Job time : 133 secs
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:22:24 ; Search time 18 Seconds
(without alignments)
21.950 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 396018 seqs, 79020188 residues

Total number of hits satisfying chosen parameters: 1401

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14	70.0	5	5	US-09-281-717A-3	Sequence 3, Appli
2	11	55.0	5	1	PCT-US02-32657-65	Sequence 65, Appl
3	11	55.0	5	1	PCT-US02-33556-34	Sequence 34, Appl
4	11	55.0	5	1	PCT-US02-33556-36	Sequence 36, Appl
5	11	55.0	5	1	PCT-US02-33556-40	Sequence 40, Appl
6	11	55.0	5	1	PCT-US02-33985-2	Sequence 2, Appli
7	11	55.0	5	1	PCT-US02-34760-21	Sequence 21, Appl
8	11	55.0	5	1	PCT-US02-34760-46	Sequence 46, Appl
9	11	55.0	5	1	PCT-US02-34760-47	Sequence 47, Appl
10	11	55.0	5	1	PCT-US02-35606-2	Sequence 2, Appli
11	11	55.0	5	1	PCT-US02-16525A-26	Sequence 26, Appl
12	11	55.0	5	1	PCT-US02-24469-21	Sequence 21, Appl
13	11	55.0	5	1	PCT-US02-24310-166	Sequence 166, App
14	11	55.0	5	1	PCT-US02-24469A-21	Sequence 21, Appl
15	11	55.0	5	1	PCT-US02-39109-15	Sequence 15, Appl
16	11	55.0	5	1	PCT-US02-32307-23	Sequence 23, Appl
17	11	55.0	5	1	PCT-US02-39643-5	Sequence 5, Appli
18	11	55.0	5	4	US-08-832-443C-13	Sequence 13, Appl
19	11	55.0	5	5	US-09-721-456-540	Sequence 540, App
20	11	55.0	5	5	US-09-533-800-16	Sequence 16, Appl
21	11	55.0	5	5	US-09-813-484-1	Sequence 1, Appli
22	11	55.0	5	5	US-09-726-348B-5	Sequence 5, Appli
23	11	55.0	5	5	US-09-653-812B-145	Sequence 145, App
24	11	55.0	5	5	US-09-653-812B-152	Sequence 152, App
25	11	55.0	5	5	US-09-556-972-12	Sequence 12, Appl
26	11	55.0	5	5	US-09-610-650B-18	Sequence 18, Appl
27	11	55.0	5	5	US-09-943-120-1	Sequence 1, Appli
28	11	55.0	5	5	US-09-936-759-32	Sequence 32, Appl
29	11	55.0	5	5	US-09-969-748C-19	Sequence 19, Appl
30	11	55.0	5	5	US-09-969-748C-20	Sequence 20, Appl
31	11	55.0	5	5	US-09-553-800D-16	Sequence 16, Appl
32	11	55.0	5	5	US-09-720-278A-1	Sequence 1, Appli
33	11	55.0	5	5	US-09-720-278A-2	Sequence 2, Appli
34	11	55.0	5	5	US-09-720-278A-3	Sequence 3, Appli
35	11	55.0	5	5	US-09-720-278A-5	Sequence 5, Appli
36	11	55.0	5	5	US-09-720-278A-21	Sequence 21, Appl
37	11	55.0	5	5	US-09-720-278A-23	Sequence 23, Appl
38	11	55.0	5	5	US-09-720-278A-27	Sequence 27, Appl
39	11	55.0	5	5	US-09-636-243B-30	Sequence 30, Appl
40	11	55.0	5	5	US-09-636-243B-35	Sequence 35, Appl
41	11	55.0	5	5	US-09-636-243B-44	Sequence 44, Appl
42	11	55.0	5	5	US-09-636-243B-56	Sequence 56, Appl
43	11	55.0	5	5	US-09-636-243B-57	Sequence 57, Appl
44	11	55.0	5	5	US-09-636-243B-58	Sequence 58, Appl
45	11	55.0	5	5	US-09-636-243B-59	Sequence 59, Appl

ALIGNMENTS

```
RESULT 1
US-09-281-717A-3
; Sequence 3, Application US/09281717A
; GENERAL INFORMATION:
;  APPLICANT: Baxter, John
;  APPLICANT:  Darimont, Beatrice
;  APPLICANT:  Feng, Weijun
;  APPLICANT:  Fletterick, Robert
;  APPLICANT:  Kushner, Peter
;  APPLICANT:  West, Brian
;  APPLICANT:  Wagner, Richard
;  APPLICANT:  Yamamoto, Keith
;  TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
;  TITLE OF INVENTION:  COACTIVAOR BINDING
;  FILE REFERENCE: 9811-008-999
;  CURRENT APPLICATION NUMBER: US/09/281,717A
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: US 60/079,956
;  PRIOR FILING DATE: 1998-03-30
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Variant
;   LOCATION: (2)..(3)
;   OTHER INFORMATION: Xaa is any amino acid
US-09-281-717A-3

  Query Match             70.0%;  Score 14;  DB 5;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |||.|
Db       1 FXXLW 5


RESULT 2
PCT-US02-32657-65
; Sequence 65, Application PC/TUS0232657
; GENERAL INFORMATION:
;  APPLICANT: AMGEN INC.
;  TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
;  FILE REFERENCE: A-801B
;  CURRENT APPLICATION NUMBER: PCT/US02/32657
;  CURRENT FILING DATE:  2002-10-11
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;  PRIOR APPLICATION NUMBER: US 60/414,155
;  PRIOR FILING DATE: 2002-09-27
;  PRIOR APPLICATION NUMBER: US 60/328,624
;  PRIOR FILING DATE: 2001-10-11
;  NUMBER OF SEQ ID NOS: 359
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polypeptide capable of binding to Ang-2
PCT-US02-32657-65

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
           |
Db       1 W 1


RESULT 3
PCT-US02-33556-34
; Sequence 34, Application PC/TUS0233556
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
;  TITLE OF INVENTION:  Neutralizing Activity
;  FILE REFERENCE: A-799
;  CURRENT APPLICATION NUMBER: PCT/US02/33556
;  CURRENT FILING DATE:  2002-10-17
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-33556-34

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
           |
Db       4 W 4


RESULT 4
PCT-US02-33556-36
; Sequence 36, Application PC/TUS0233556
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
;  TITLE OF INVENTION:  Neutralizing Activity
;  FILE REFERENCE: A-799
;  CURRENT APPLICATION NUMBER: PCT/US02/33556
;  CURRENT FILING DATE:  2002-10-17
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-33556-36

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
           |
Db       4 W 4


RESULT 5
PCT-US02-33556-40
; Sequence 40, Application PC/TUS0233556
; GENERAL INFORMATION:
;  APPLICANT: Amgen, Inc.
;  TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
;  TITLE OF INVENTION:  Neutralizing Activity
;  FILE REFERENCE: A-799
;  CURRENT APPLICATION NUMBER: PCT/US02/33556
;  CURRENT FILING DATE:  2002-10-17
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-33556-40

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
           |
Db       4 W 4


RESULT 6
PCT-US02-33985-2
; Sequence 2, Application PC/TUS0233985
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: 16 Human Secreted Proteins
;  FILE REFERENCE: PS739PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/33985
;  CURRENT FILING DATE:  2002-10-24
;  PRIOR APPLICATION NUMBER: 60/330,629
;  PRIOR FILING DATE: 2001-10-26
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Site
;   LOCATION: (3)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
PCT-US02-33985-2

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
           |
Db       1 W 1


RESULT 7
PCT-US02-34760-21
; Sequence 21, Application PC/TUS0234760
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT:  Haviv, Fortuna
;  APPLICANT:  Bradley, Michael F.
;  TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES
;  TITLE OF INVENTION:  HAVING ANTIANGIOGENIC ACTIVITY
;  FILE REFERENCE: 6854.WO.01
```

```
;  CURRENT APPLICATION NUMBER: PCT/US02/34760
;  CURRENT FILING DATE:  2002-10-30
;  PRIOR APPLICATION NUMBER: 10/263,811
;  PRIOR FILING DATE: 2002-10-04
;  PRIOR APPLICATION NUMBER: 10/000,540
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 10/000,007
;  PRIOR FILING DATE: 2001-10-31
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antiangiogenic Peptide
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (2)...(2)
;   OTHER INFORMATION: Xaa = Nva at position 2
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (5)...(5)
;   OTHER INFORMATION: Xaa = prolylethylamide at position 5
PCT-US02-34760-21

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
           |
Db       1 W 1


RESULT 8
PCT-US02-34760-46
; Sequence 46, Application PC/TUS0234760
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT:  Haviv, Fortuna
;  APPLICANT:  Bradley, Michael F.
;  TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES
;  TITLE OF INVENTION:  HAVING ANTIANGIOGENIC ACTIVITY
;  FILE REFERENCE: 6854.WO.01
;  CURRENT APPLICATION NUMBER: PCT/US02/34760
;  CURRENT FILING DATE:  2002-10-30
;  PRIOR APPLICATION NUMBER: 10/263,811
;  PRIOR FILING DATE: 2002-10-04
;  PRIOR APPLICATION NUMBER: 10/000,540
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 10/000,007
;  PRIOR FILING DATE: 2001-10-31
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antiangiogenic Peptide
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (5)...(5)
;   OTHER INFORMATION: Xaa = proethylamide at position 5
PCT-US02-34760-46

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
           |
Db       2 W 2


RESULT 9
PCT-US02-34760-47
; Sequence 47, Application PC/TUS0234760
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT:  Haviv, Fortuna
;  APPLICANT:  Bradley, Michael F.
;  TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES
;  TITLE OF INVENTION:  HAVING ANTIANGIOGENIC ACTIVITY
;  FILE REFERENCE: 6854.WO.01
;  CURRENT APPLICATION NUMBER: PCT/US02/34760
;  CURRENT FILING DATE:  2002-10-30
;  PRIOR APPLICATION NUMBER: 10/263,811
;  PRIOR FILING DATE: 2002-10-04
;  PRIOR APPLICATION NUMBER: 10/000,540
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: 10/000,007
;  PRIOR FILING DATE: 2001-10-31
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antiangiogenic Peptide
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (5)...(5)
;   OTHER INFORMATION: Xaa = proethylamide at position 5
PCT-US02-34760-47

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
           |
Db       2 W 2


RESULT 10
PCT-US02-35606-2
; Sequence 2, Application PC/TUS0235606
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: 41 Human Secreted Proteins
;  FILE REFERENCE: PS740PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/35606
;  CURRENT FILING DATE:  2002-11-06
;  PRIOR APPLICATION NUMBER: 60/331,046
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 160
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Site
;   LOCATION: (3)
;   OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring L-amino acids
PCT-US02-35606-2

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 W 5
           |
```

```
Db      1 W 1


RESULT 11
PCT-US02-16525A-26
; Sequence 26, Application PC/TUS0216525A
; GENERAL INFORMATION:
;  APPLICANT: Bell et al.
;  TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
;  FILE REFERENCE: PF556PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/16525A
;  CURRENT FILING DATE:  2002-05-24
;  PRIOR APPLICATION NUMBER: 60/293,212
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 137
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (3)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US02-16525A-26

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
          |
Db      1 W 1


RESULT 12
PCT-US02-24469-21
; Sequence 21, Application PC/TUS0224469
; GENERAL INFORMATION:
;  APPLICANT: Merck & Co., Inc.
;  TITLE OF INVENTION: Biological Assay Detection Method
;  FILE REFERENCE: PCT 20900Y
;  CURRENT APPLICATION NUMBER: PCT/US02/24469
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: 60/310,599
;  PRIOR FILING DATE: 2001-08-07
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Xaa is a variable which may be
;   OTHER INFORMATION: A,R,N,D,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(5)
;   OTHER INFORMATION: Xaa = Any Amino Acid
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(5)
;   OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-24469-21

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
          |
Db      3 W 3


RESULT 13
PCT-US02-24310-166
; Sequence 166, Application PC/TUS0224310
; GENERAL INFORMATION:
;  APPLICANT: CUBIST PHARMACEUTICALS, INC.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
;  TITLE OF INVENTION:  BIOSYNTHETIC GENE CLUSTER
;  FILE REFERENCE: CUB-12 PCT CIP
;  CURRENT APPLICATION NUMBER: PCT/US02/24310
;  CURRENT FILING DATE:  2002-10-25
;  PRIOR APPLICATION NUMBER: PCT/US01/32354
;  PRIOR FILING DATE: 2001-10-17
;  PRIOR APPLICATION NUMBER: 60/310,385
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: 60/379,866
;  PRIOR FILING DATE: 2002-05-10
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 166
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Illustrative
;   OTHER INFORMATION: thioesterase motif
PCT-US02-24310-166

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
          |
Db      2 W 2


RESULT 14
PCT-US02-24469A-21
; Sequence 21, Application PC/TUS0224469A
; GENERAL INFORMATION:
;  APPLICANT: Merck & Co., Inc.
;  TITLE OF INVENTION: Biological Assay Detection Method
;  FILE REFERENCE: PCT 20900Y
;  CURRENT APPLICATION NUMBER: PCT/US02/24469A
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: 60/310,599
;  PRIOR FILING DATE: 2001-08-07
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Xaa is a variable which may be
;   OTHER INFORMATION: A,R,N,D,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(5)
;   OTHER INFORMATION: Xaa = Any Amino Acid
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(5)
;   OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-24469A-21

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
          |
```

```
Db      3 W 3


RESULT 15
PCT-US02-39109-15
; Sequence 15, Application PC/TUS0239109
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as represented by the
;  APPLICANT:  Secretary, Department of Health and Human Services
;  APPLICANT:  Ruscetti, Francis W.
;  APPLICANT:  Ruff, Michael R.
;  TITLE OF INVENTION: PEPTIDE T STIMULATES CTL RESPONSES
;  FILE REFERENCE: 14014.0404P1
;  CURRENT APPLICATION NUMBER: PCT/US02/39109
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: 60/338,971
;  PRIOR FILING DATE: 2001-12-07
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/note =
;   OTHER INFORMATION: Synthetic Construct
PCT-US02-39109-15

  Query Match             55.0%;  Score 11;  DB 1;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    1;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 W 5
          |
Db      3 W 3


Search completed: January 29, 2003, 14:26:20
Job time : 18 secs
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OM protein - protein search, using sw model

Run on: January 29, 2003, 14:21:29 ; Search time 14 Seconds
(without alignments)
10.508 Million cell updates/sec

Title: US-09-403-440A-4
Perfect score: 20
Sequence: 1 FXXXW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 10533

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14	70.0	5	1	US-08-424-957-4	Sequence 4, Appli
2	14	70.0	5	1	US-08-424-957-5	Sequence 5, Appli
3	14	70.0	5	3	US-08-981-122-37	Sequence 37, Appl
4	14	70.0	5	4	US-09-035-686-4	Sequence 4, Appli
5	14	70.0	5	4	US-09-035-686-5	Sequence 5, Appli
6	14	70.0	5	4	US-09-099-053-3	Sequence 3, Appli
7	13	65.0	5	1	US-08-064-111C-22	Sequence 22, Appl
8	13	65.0	5	1	US-07-789-184-83	Sequence 83, Appl
9	13	65.0	5	1	US-08-475-263-83	Sequence 83, Appl
10	13	65.0	5	1	US-08-485-886-83	Sequence 83, Appl
11	13	65.0	5	2	US-08-477-362-83	Sequence 83, Appl
12	13	65.0	5	2	US-08-477-134-83	Sequence 83, Appl
13	13	65.0	5	3	US-08-473-489A-83	Sequence 83, Appl
14	13	65.0	5	3	US-08-485-695-83	Sequence 83, Appl
15	13	65.0	5	3	US-08-981-122-2	Sequence 2, Appli
16	13	65.0	5	4	US-08-018-760-83	Sequence 83, Appl
17	11	55.0	5	1	US-07-657-769B-15	Sequence 15, Appl
18	11	55.0	5	1	US-07-657-769B-16	Sequence 16, Appl
19	11	55.0	5	1	US-07-657-769B-17	Sequence 17, Appl
20	11	55.0	5	1	US-07-657-769B-18	Sequence 18, Appl
21	11	55.0	5	1	US-07-657-769B-19	Sequence 19, Appl
22	11	55.0	5	1	US-07-657-769B-20	Sequence 20, Appl
23	11	55.0	5	1	US-07-657-769B-21	Sequence 21, Appl
24	11	55.0	5	1	US-07-657-769B-22	Sequence 22, Appl
25	11	55.0	5	1	US-07-657-769B-36	Sequence 36, Appl
26	11	55.0	5	1	US-07-657-769B-37	Sequence 37, Appl
27	11	55.0	5	1	US-07-657-769B-38	Sequence 38, Appl
28	11	55.0	5	1	US-07-657-769B-39	Sequence 39, Appl
29	11	55.0	5	1	US-07-801-388-5	Sequence 5, Appli
30	11	55.0	5	1	US-07-792-259-9	Sequence 9, Appli
31	11	55.0	5	1	US-07-858-842-3	Sequence 3, Appli
32	11	55.0	5	1	US-07-893-930-1	Sequence 1, Appli
33	11	55.0	5	1	US-07-893-930-2	Sequence 2, Appli
34	11	55.0	5	1	US-07-893-930-3	Sequence 3, Appli
35	11	55.0	5	1	US-07-893-930-4	Sequence 4, Appli
36	11	55.0	5	1	US-07-893-930-5	Sequence 5, Appli
37	11	55.0	5	1	US-07-893-930-6	Sequence 6, Appli
38	11	55.0	5	1	US-07-893-930-7	Sequence 7, Appli
39	11	55.0	5	1	US-07-893-930-8	Sequence 8, Appli
40	11	55.0	5	1	US-07-893-930-9	Sequence 9, Appli
41	11	55.0	5	1	US-07-893-930-10	Sequence 10, Appl
42	11	55.0	5	1	US-07-893-930-11	Sequence 11, Appl
43	11	55.0	5	1	US-07-893-930-12	Sequence 12, Appl
44	11	55.0	5	1	US-07-893-930-13	Sequence 13, Appl
45	11	55.0	5	1	US-07-893-930-25	Sequence 25, Appl

ALIGNMENTS

```
RESULT 1
US-08-424-957-4
; Sequence 4, Application US/08424957
; Patent No. 5770377
;  GENERAL INFORMATION:
;    APPLICANT:  Picksley, Steven M.
;    APPLICANT:  Lane, David P.
;    TITLE OF INVENTION:  Interruption of Binding of MDM2 and P53
;    TITLE OF INVENTION:  Protein and Therapeutic Application Thereof
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/424,957
;      FILING DATE:  19-APR-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,660
;      FILING DATE:  20-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-61228/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
US-08-424-957-4

  Query Match             70.0%;  Score 14;  DB 1;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
```

```
          ||| |
Db      1 FXXLW 5


RESULT 2
US-08-424-957-5
; Sequence 5, Application US/08424957
; Patent No. 5770377
;  GENERAL INFORMATION:
;    APPLICANT:  Picksley, Steven M.
;    APPLICANT:  Lane, David P.
;    TITLE OF INVENTION:  Interruption of Binding of MDM2 and P53
;    TITLE OF INVENTION:  Protein and Therapeutic Application Thereof
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/424,957
;      FILING DATE:  19-APR-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/277,660
;      FILING DATE:  20-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-61228/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
US-08-424-957-5

  Query Match             70.0%;  Score 14;  DB 1;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.9e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          ||  |
Db      1 FXELW 5


RESULT 3
US-08-981-122-37
; Sequence 37, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
;  APPLICANT:  Hatanaka, Yoshihiro
;  APPLICANT:  Aritomi, Masaharu
;  TITLE OF INVENTION:  Peptide for binding thereto a low density lipoprotein
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/08/981,122B
;  CURRENT FILING DATE:  1997-12-18
;  PRIOR APPLICATION NUMBER:  JP 7-176904
;  PRIOR FILING DATE:  1995-06-21
;  PRIOR APPLICATION NUMBER:  PCT/JP96/01734
;  PRIOR FILING DATE:  1996-06-21
;  NUMBER OF SEQ ID NOS:  90
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 37
;    LENGTH: 5
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    NAME/KEY: AMIDATION
;    LOCATION: 5
;    OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-
; Patent No. 6127339
;    OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic pep
;    OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
US-08-981-122-37

  Query Match             70.0%;  Score 14;  DB 3;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 FXXXW 5
          |   |
Db      1 FFFRW 5


RESULT 4
US-09-035-686-4
; Sequence 4, Application US/09035686
; Patent No. 6153391
;  GENERAL INFORMATION:
;    APPLICANT:  Picksley, Steven M.
;    APPLICANT:  Lane, David P.
;    TITLE OF INVENTION:  Interruption of Binding of MDM2 and P53
;    TITLE OF INVENTION:  Protein and Therapeutic Application Thereof
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/035,686
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/424,957
;      FILING DATE:  19-APR-1995
;      APPLICATION NUMBER:  US 08/277,660
;      FILING DATE:  20-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-61228/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
US-09-035-686-4

  Query Match             70.0%;  Score 14;  DB 4;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+05;
```

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  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           ||| |
Db       1 FXXLW 5


RESULT 5
US-09-035-686-5
; Sequence 5, Application US/09035686
; Patent No. 6153391
;  GENERAL INFORMATION:
;    APPLICANT:  Picksley, Steven M.
;    APPLICANT:  Lane, David P.
;    TITLE OF INVENTION:  Interruption of Binding of MDM2 and P53
;    TITLE OF INVENTION:  Protein and Therapeutic Application Thereof
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/035,686
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/424,957
;      FILING DATE:  19-APR-1995
;      APPLICATION NUMBER:  US 08/277,660
;      FILING DATE:  20-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-61228/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
US-09-035-686-5

  Query Match             70.0%;  Score 14;  DB 4;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.9e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           ||  |
Db       1 FXELW 5


RESULT 6
US-09-099-053-3
; Sequence 3, Application US/09099053
; Patent No. 6388063
;  GENERAL INFORMATION:
;    APPLICANT:  Greg Plowman
;    APPLICANT:  Susan Onrust
;    APPLICANT:  David Markby
;    APPLICANT:  Sara Courtneidge
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF
;    TITLE OF INVENTION:  SAD RELATED DISORDERS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/099,053
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/049,914
;      FILING DATE:  June 18, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  235/121
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      OTHER INFORMATION:  "Xaa" in position 3 stands for
;      OTHER INFORMATION:  either Glu or Asp.
US-09-099-053-3

  Query Match             70.0%;  Score 14;  DB 4;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.9e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           | | |
Db       1 FGXVW 5


RESULT 7
US-08-064-111C-22
; Sequence 22, Application US/08064111C
; Patent No. 5688760
;  GENERAL INFORMATION:
;    APPLICANT:  Kemp, Bruce E.
;    APPLICANT:  Nicholson, Geoffrey C.
;    APPLICANT:  Martin, Thomas J.
;    APPLICANT:  Fenton, Anna J.
;    APPLICANT:  Hammonds, R. Glenn
;    TITLE OF INVENTION:  COMPOUNDS AND COMPOSITIONS WHICH INHIBIT
;    TITLE OF INVENTION:  BONE RESORPTION
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert,
;      ADDRESSEE:  Attn: W.H. Dreger
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
```

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/064,111C
;      FILING DATE:  12-AUG-1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/AU91/00580
;      FILING DATE:  13-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PK9567
;      FILING DATE:  19-NOV-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PK3879
;      FILING DATE:  13-DEC-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Walter H.
;      REGISTRATION NUMBER:  24,190
;      REFERENCE/DOCKET NUMBER:  A-58456/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-064-111C-22

  Query Match             65.0%;  Score 13;  DB 1;  Length 5;
  Best Local Similarity   20.0%;  Pred. No. 1.9e+05;
  Matches    1;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           :   |
Db       1 YRSAW 5


RESULT 8
US-07-789-184-83
; Sequence 83, Application US/07789184
; Patent No. 5688768
;  GENERAL INFORMATION:
;    APPLICANT:  COUGHLIN, SHAUN R.
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  RECOMBINANT THROMBIN RECEPTOR AND
;    TITLE OF INVENTION:  RELATED PHARMACEUTICALS
;    NUMBER OF SEQUENCES:  223
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/789,184
;      FILING DATE:  19911107
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22000-20502.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  34-0154
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-789-184-83

  Query Match             65.0%;  Score 13;  DB 1;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FEPFW 5


RESULT 9
US-08-475-263-83
; Sequence 83, Application US/08475263
; Patent No. 5759994
;  GENERAL INFORMATION:
;    APPLICANT:  COUGHLIN, SHAUN R.
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  RECOMBINANT THROMBIN RECEPTOR AND
;    TITLE OF INVENTION:  RELATED PHARMACEUTICALS
;    NUMBER OF SEQUENCES:  223
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Ave., NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,263
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22000-20502.03
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-475-263-83

  Query Match             65.0%;  Score 13;  DB 1;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FEPFW 5
```

```
RESULT 10
US-08-485-886-83
; Sequence 83, Application US/08485886
; Patent No. 5798248
;  GENERAL INFORMATION:
;    APPLICANT:  COUGHLIN, SHAUN R.
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  RECOMBINANT THROMBIN RECEPTOR AND
;    TITLE OF INVENTION:  RELATED PHARMACEUTICALS
;    NUMBER OF SEQUENCES:  223
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,886
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/789,184
;      FILING DATE:  07-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22000-20502.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  34-0154
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-485-886-83

  Query Match             65.0%;  Score 13;  DB 1;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |  |
Db       1 FEPFW 5


RESULT 11
US-08-477-362-83
; Sequence 83, Application US/08477362
; Patent No. 5849507
;  GENERAL INFORMATION:
;    APPLICANT:  COUGHLIN, SHAUN R.
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  RECOMBINANT THROMBIN RECEPTOR AND
;    TITLE OF INVENTION:  RELATED PHARMACEUTICALS
;    NUMBER OF SEQUENCES:  223
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,362
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/789,184
;      FILING DATE:  07-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22000-20502.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  34-0154
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-477-362-83

  Query Match             65.0%;  Score 13;  DB 2;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |  |
Db       1 FEPFW 5


RESULT 12
US-08-477-134-83
; Sequence 83, Application US/08477134
; Patent No. 5856448
;  GENERAL INFORMATION:
;    APPLICANT:  COUGHLIN, SHAUN R.
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  RECOMBINANT THROMBIN RECEPTOR AND
;    TITLE OF INVENTION:  RELATED PHARMACEUTICALS
;    NUMBER OF SEQUENCES:  223
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,134
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/789,184
;      FILING DATE:  07-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22000-20502.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  34-0154
;  INFORMATION FOR SEQ ID NO:  83:
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```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-477-134-83

  Query Match             65.0%;  Score 13;  DB 2;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FEPFW 5


RESULT 13
US-08-473-489A-83
; Sequence 83, Application US/08473489A
; Patent No. 6024936
;  GENERAL INFORMATION:
;    APPLICANT:  COUGHLIN, SHAUN R.
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  RECOMBINANT THROMBIN RECEPTOR AND
;    TITLE OF INVENTION:  RELATED PHARMACEUTICALS
;    NUMBER OF SEQUENCES:  223
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/473,489A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/789,184
;      FILING DATE:  1991-11-07
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22000-20502.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  34-0154
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-473-489A-83

  Query Match             65.0%;  Score 13;  DB 3;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FEPFW 5


RESULT 14
US-08-485-695-83
; Sequence 83, Application US/08485695
; Patent No. 6124101
;  GENERAL INFORMATION:
;    APPLICANT:  COUGHLIN, SHAUN R.
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  RECOMBINANT THROMBIN RECEPTOR AND
;    TITLE OF INVENTION:  RELATED PHARMACEUTICALS
;    NUMBER OF SEQUENCES:  223
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,695
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/789,184
;      FILING DATE:  07-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22000-20502.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  34-0154
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-485-695-83

  Query Match             65.0%;  Score 13;  DB 3;  Length 5;
  Best Local Similarity   40.0%;  Pred. No. 1.9e+05;
  Matches    2;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 FXXXW 5
           |   |
Db       1 FEPFW 5


RESULT 15
US-08-981-122-2
; Sequence 2, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
;  APPLICANT:  Hatanaka, Yoshihiro
;  APPLICANT:  Aritomi, Masaharu
;  TITLE OF INVENTION:  Peptide for binding thereto a low density lipoprotein
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/08/981,122B
;  CURRENT FILING DATE:  1997-12-18
;  PRIOR APPLICATION NUMBER:  JP 7-176904
;  PRIOR FILING DATE:  1995-06-21
;  PRIOR APPLICATION NUMBER:  PCT/JP96/01734
;  PRIOR FILING DATE:  1996-06-21
;  NUMBER OF SEQ ID NOS:  90
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
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; OTHER INFORMATION: Sequence of a peptide synthesized in Example 1 from L-form
; Patent No. 6127339
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multipeptide
; OTHER INFORMATION: synthesizing system (RaMPS)
US-08-981-122-2

Query Match 65.0%; Score 13; DB 3; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1 FXXXW 5
           |   |
Db       1 FKIWW 5
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Search completed: January 29, 2003, 14:23:38
Job time : 15 secs